

FIG. 1A

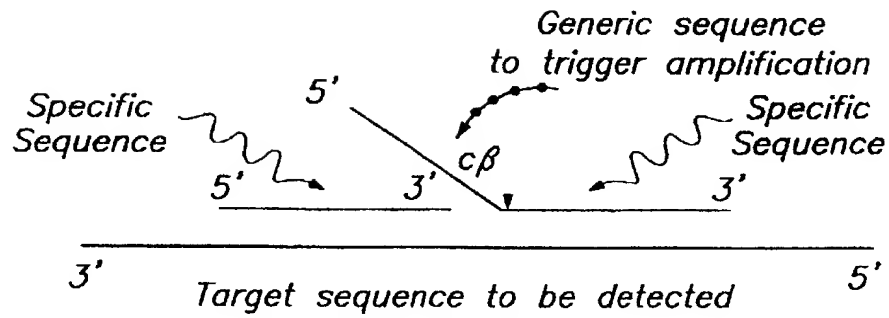


FIG. 1B PART ONE: TRIGGER REACTION

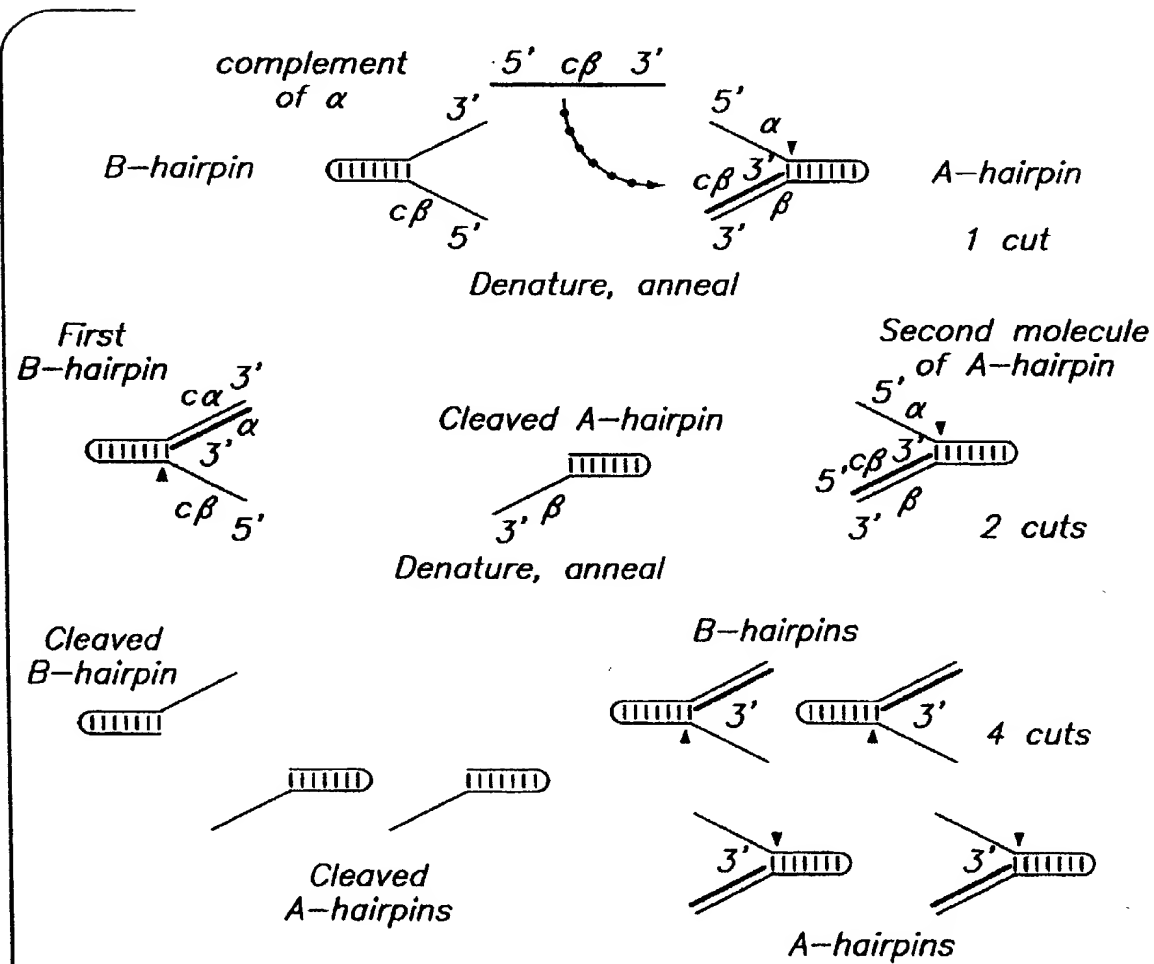


FIG. 1C PART TWO: DETECTION REACTION

THE UNIVERSITY OF CHICAGO

DNAPTAQ [SEQ ID NO:1]	...	AG	G	...	G	...	70
DNAPTFL [SEQ ID NO:2]	C	G	67
DNAPTTE [SEQ ID NO:3]	...	GA	G	A	70

DNAPTAO	CA.	G. G.	140
DNAPTFL	T.	C.	137
DNAPTTH		G.	140

ONAPTAQ	C.	...	A.	207
ONAPTEL	A.	OT.	T.	204
ONAPTTA	T.	AA.	C. CT.	210

DNAPIAO	G. CG.	6.	277
DNAPIFL			274
DNAPIIH	GA.	6.	280

[illegible]

$$\frac{1}{\Gamma(\alpha)} \int_0^t (t-\tau)^{\alpha-1} f(\tau) d\tau = \frac{1}{\Gamma(\alpha)} \int_0^t (t-\tau)^{\alpha-1} f(\tau) d\tau$$

ONAPTAQ [SEQ ID NO:1]	C.	G.	C.	417
ONAPTFL [SEQ ID NO:2]	T.	G.	C.G.	414
ONAPTTH [SEQ ID NO:3]	.	T.	C.	420

DNAPTAC	AAA.	T.	GA.	487
DNAPTFL	T.		G. G.	484
DNAPTTH		A.	G. G.	490

DNAPIAQ	C.	A.	C. C.	CG.	A.	557
DNAPIFL		AC.	C. C.			554
DNAPIIH	A.		C.	T.	C. T	560

ONAPIAG	C.....GAG.....T.....G.GAG.....T..GG..	627
ONAPIELG.T...A.....G.....A.G...A..GGC	624
ONAPIIRT.....T.....T.....T.....A.....A.....	630

.....	GC.....	C.....	A.....	694
.....	T.C.C.....	A.....	T.....	T.C.....	C.....	691
.....						700

[illegible]

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(Faint, illegible text from bleed-through)

FIG. 2E

MAJORITY [SEQ ID NO:7]		GGAGATCGCGCGCCCTCGAGGAGGAGGCTCTTGGGCTTGGCGGGCCACCCCTTCAAGCTCAAGTCCGCGGGAC	
DNAPTAQ [SEQ ID NO:1]	GC	CC	1484
DNAPTFL [SEQ ID NO:2]	G. G. AG. G.		1461
DNAPTTH [SEQ ID NO:3]	T. G.		1470
MAJORITY		CAGCTGGAAAGGCTCTTGCAGGAGCTXGGGCTTCCCGGCATCGGCAAGACGGAGAGACXGGCAAGC	
DNAPTAQ	G.	A.	1534
DNAPTFL	GC.	G. C. G. T.	1531
DNAPTTH	TA.	T. G. G. C. A.	1540
MAJORITY		GCTCCAGCAGCGCGCGCGCTGCTGGAGGGGCTXGCGAGGGCCAGCCCATCGTGGAGAGATCCTGCAGTA	
DNAPTAQ	G.	C.	1604
DNAPTFL	T.	G. A.	1601
DNAPTTH	G.	A. G.	1610
MAJORITY		CGGGGAGGCTCAGCAAGCTCAAGAACACCTACATXGACCGCGCTGCCXGCGCTCGTCCACCGCAGGACGGGGC	
DNAPTAQ	G. G.	T. G. A.	1674
DNAPTFL	A.	G. C. G.	1671
DNAPTTH	G. G.	C. AAG.	1680
MAJORITY		CGGCTCCACACCCGCTTCAACGAGACGGCCACGGCCAGGGCTTAGTACCTCCGACCCCAACCTGC	
DNAPTAQ		A.	1744
DNAPTFL	G.	C. TCG.	1741
DNAPTTH		G.	1750

CGGCTCCACACCCGCTTCAACGAGACGGCCACGGCCAGGGCTTAGTACCTCCGACCCCAACCTGC

FIG. 2F

```

MAJORITY [SEQ ID NO:7] AGAACATCCCCGTCCGACCCXCCTGCGCCAGAGGATCCGCGCGGGGCTTCGTGGCCGAGGAGGGGTGGGT
DNAPTAQ [SEQ ID NO:1] .....G..T..G.....A.C.....G...C. 1814
DNAPTFL [SEQ ID NO:2] .....G.....T.....C.C.....A.....C.....C..... 1817
DNAPTTH [SEQ ID NO:3] .....GT.....C.....C.....T.....C.....T.....C 1820

MAJORITY GTTGGTGGCCCTGGACTATAGCCAGATAGAGGCTCGGGGTCCTGGCGGAGGCTCTCGGGGACGAGAAAGCTG
DNAPTAQ A.....T.....A.....G.....C..... 1884
DNAPTFL C.....T.....C.....T.....C..... 1881
DNAPTTH .....C.....C.....A..... 1890

MAJORITY ATCCGGGTCTCCAGAGGGGAGGACATCCACAGCCGAGAGGCGGAGCTGGATGTTGGCGGTCCCCCGGG
DNAPTAQ .....G.....GG.....G... 1954
DNAPTFL .....T.....T.....T.....C. 1951
DNAPTTH .....A.....A..... 1960

MAJORITY AGGCGGTGGACCCCTGATCGCGCGGGCGGCGCAAGACCATCAACTTCGGGCTCCTCTAGGGCATGTCCGGC
DNAPTAQ ..... 2024
DNAPTFL A.GG..A.....T.....G..... 2021
DNAPTTH .....GG.G.....G..... 2030

MAJORITY CCACGGGCTCTCCAGGAGGCTTGGCCATCCGCTACGAGGAGGGGTGGCCCTTCATTGACGGGCTACTCCAG
DNAPTAQ .....A.....T.....CCA.....T... 2094
DNAPTFL .....GG.....T..... 2091
DNAPTTH ...TA.G.....T.....A.....A 2100

```

CCGCTGAGTGGG

FIG. 2G

MAJORITY [SEQ ID NO:7]	AGCTTCCCAAGGTCCGGGCTGGATTGAGAAACCTGGAGGAGGGCAAGAGCGGGGTACGTGGAGA	2164
DNAPTAQ [SEQ ID NO:1]	2164
DNAPTFL [SEQ ID NO:2]GG.....C.CC.....T.....	2161
DNAPTTR [SEQ ID NO:3]A.A.....G.A.....C.....A.	2170
MAJORITY	CGCTCTTGGCCCGCGGCGCTACGTGCCCGAGCTCAAGCGCCGGGTGAAGAGCGTCCGGGAGCGCGCGGGA	
DNAPTAQC.....A.....AG.G.....C..	2234
DNAPTFLT.....C.....	2231
DNAPTTRAA.AA.....CA.....C.....	2240
MAJORITY	GGGCATGGCCCTTCAACATGGCCGTCCAGGGCCACCGCCGCGAGCTCATGAAGCTGGCCATGGTGAAGCTC	
DNAPTAQT.....	2304
DNAPTFLG.....CG...T	2301
DNAPTTRC.....	2310
MAJORITY	TTCGCCCGGCTXCAGGAAATCGGGGCCAGGATGGTGGTXXCAGGTCCAGGAGAGGTGGTCCCGAGGCGCG	
DNAPTAQA...GG.....T.....	2374
DNAPTFLT...C...G...TT.G...G.....	2371
DNAPTTRC.C.G...G...C.C...C...G.....	2380
MAJORITY	CCAAAGAGCGGGCGGAGGXGGTGGCCGCTTTGGCCAAAGAGGTGATGGAGGGGGTCTATCCCGCTGGCCGT	
DNAPTAQA.....CC.....CGGC.....G.....	2444
DNAPTFLG.C...AG...A.....GG.....CAG..	2441
DNAPTTRC...C...C...A...G...C...AA.C...C.....	2450

CGCTCTTGGCCCGCGGCGCTACGTGCCCGAGCTCAAGCGCCGGGTGAAGAGCGTCCGGGAGCGCGCGGGA

FIG. 2H

MAJORITY [SEQ ID NO:7]	GGCCCTGGAGGTGGACGTGGGGATGGGGGAGGACTGGCTCTCCGCCAAGGAGTAG	
DNAPTAG [SEQ ID NO:1]A.....	GA 2499
DNAPTFL [SEQ ID NO:2]CC.....	2496
DNAPTTH [SEQ ID NO:3]T.....GT...	2505

2499 2496 2505

[illegible]

[illegible]

FIG. 3C

MAJORITY	[SEQ ID NO:8]	SFPKVRAWIEKTEEGRRRGYVETLFGRRRYVPDLNARVKSUREAAERMAFNMPVQGTAAADLKKLAMVKL	
TAQ PRO	[SEQ ID NO:4]E.....	768
TFL PRO	[SEQ ID NO:5]G.....Y.....R.....	767
TTM PRO	[SEQ ID NO:6]K.....	770
MAJORITY		FPLXEMGARM LQVHDELVL EAPKXRAEXVAALAKEVMEGVYPLAVPLEVEVGXGEDWLSAKEX	
TAQ PRO	E.....E...A...R.....I.....	833
TFL PRO	O.L.....D...R.....W.O.....L.....	831
TTM PRO	R.....L.....OA...E...A..KA.....M.....G	835

FIG. 3C



[Faint, illegible handwritten notes]



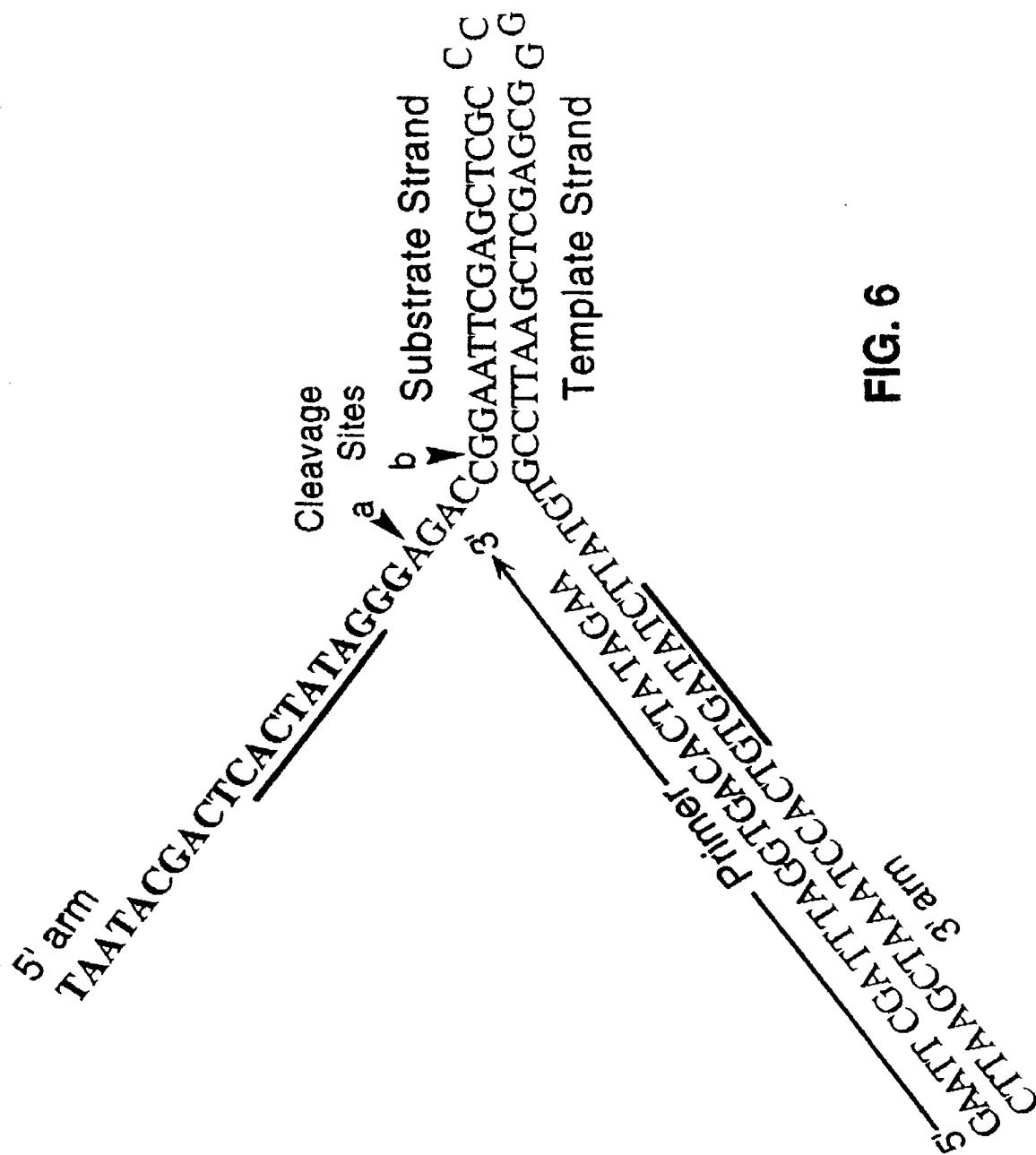


FIG. 6

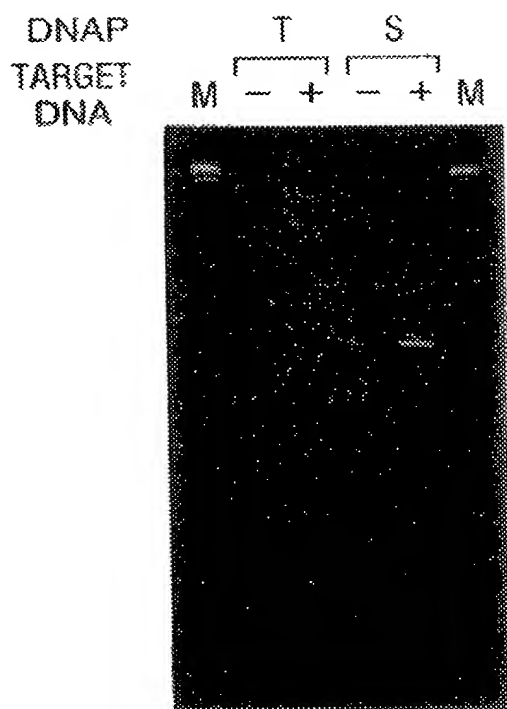


FIG. 7

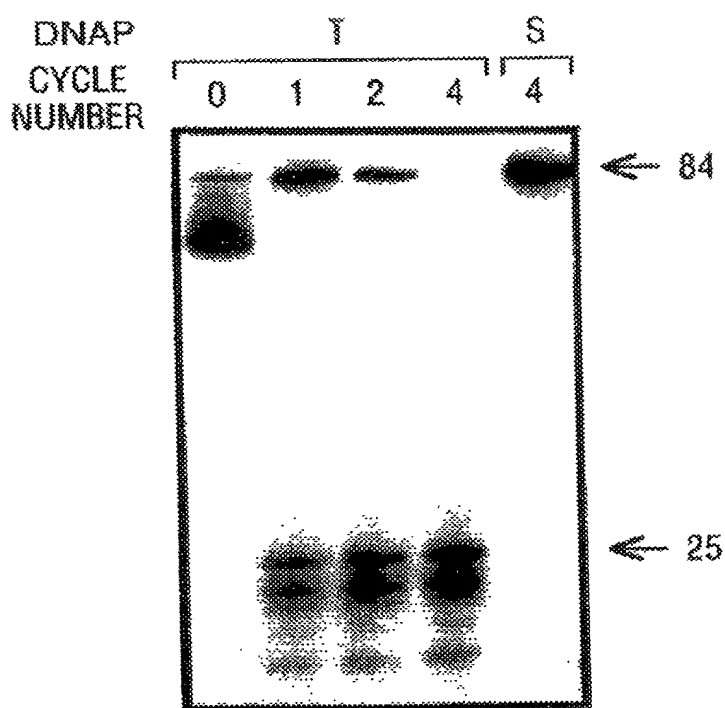


FIG. 8

	1	2	3	4	5	6
DNAP-T:	-	+	+	+	+	+
MgCl ₂ :	+	-	+	+	+	+
dNTPs:	+	-	+	-	+	-
Primers:	+	-	+	+	-	-

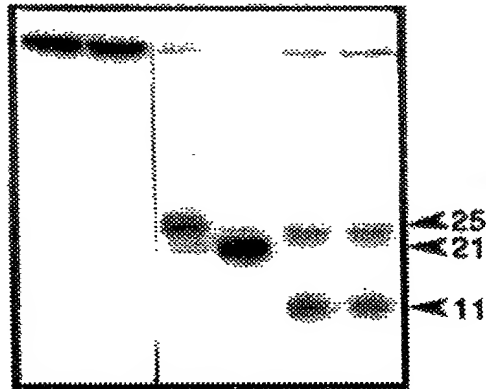


FIG. 9A

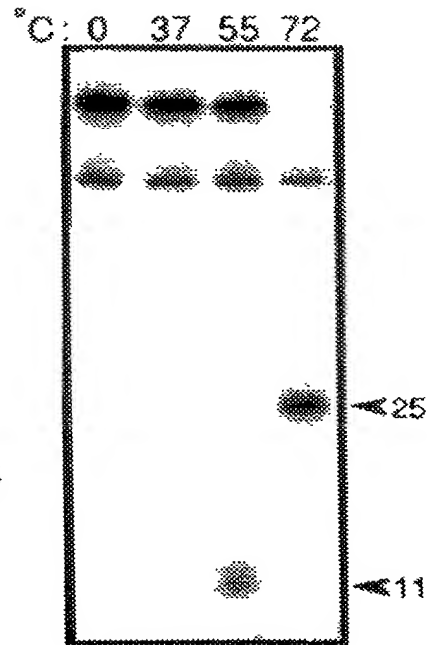


FIG. 9B

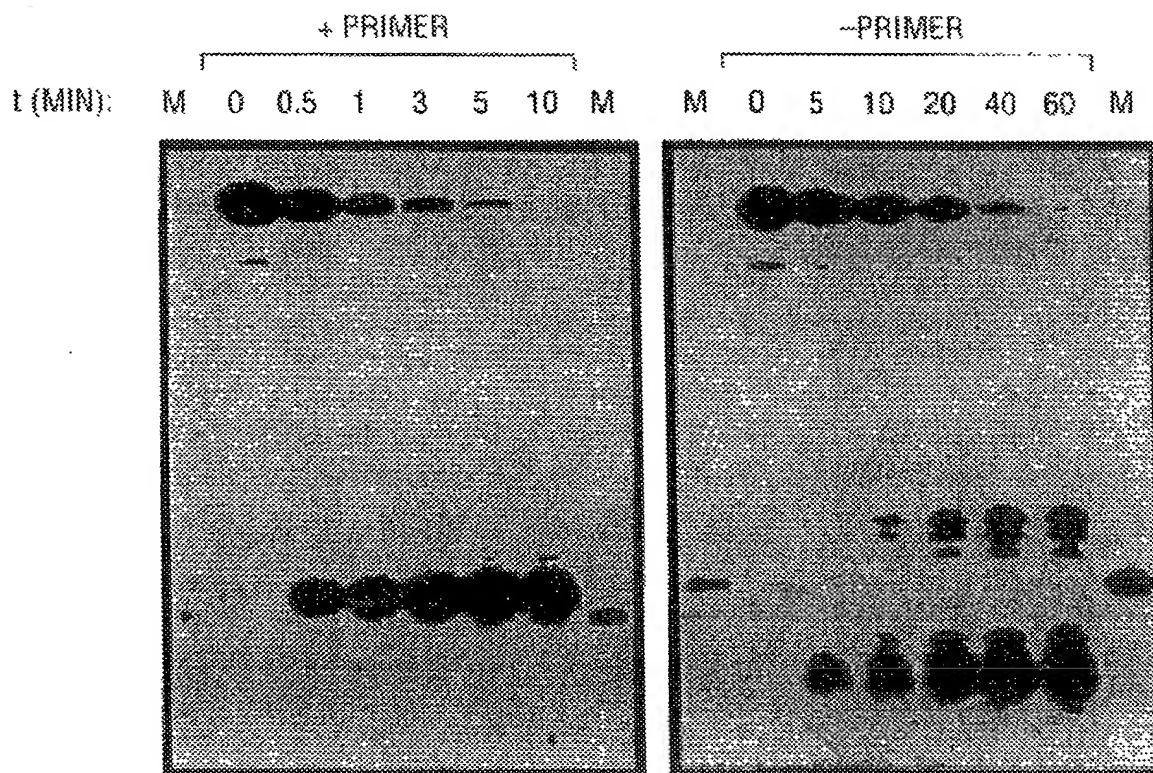


FIG. 10A

FIG. 10B

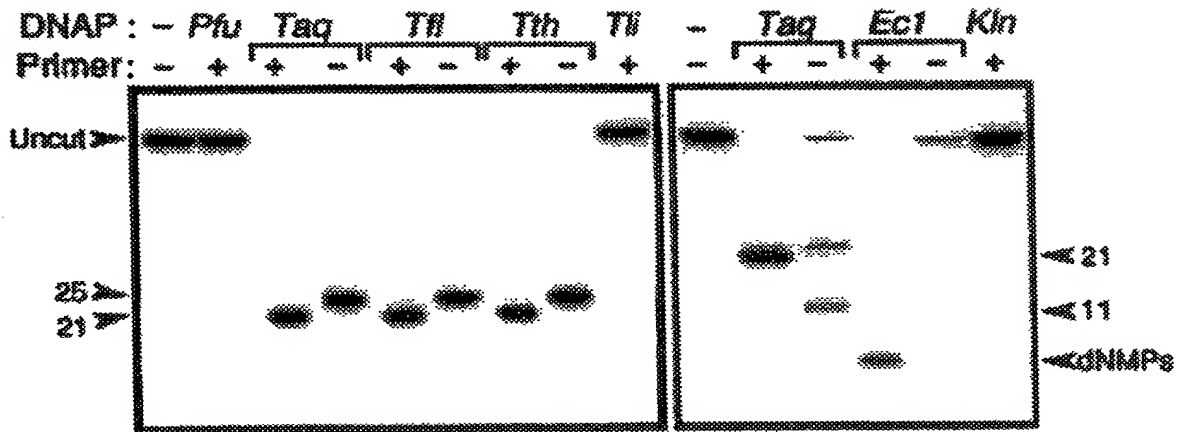
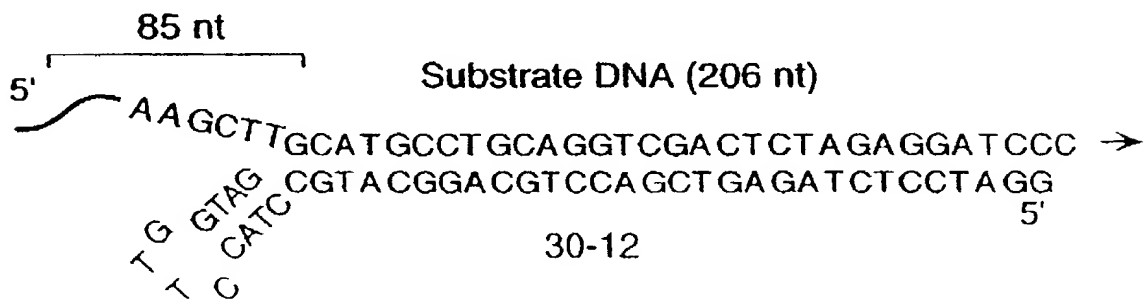
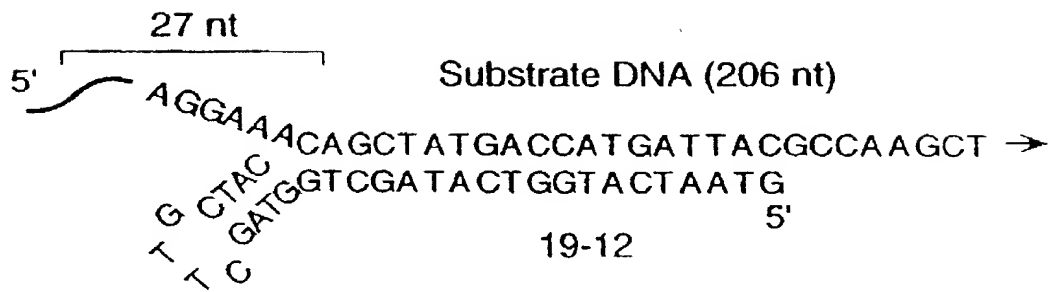


FIG. 11A

FIG. 11B

FIG. 12A



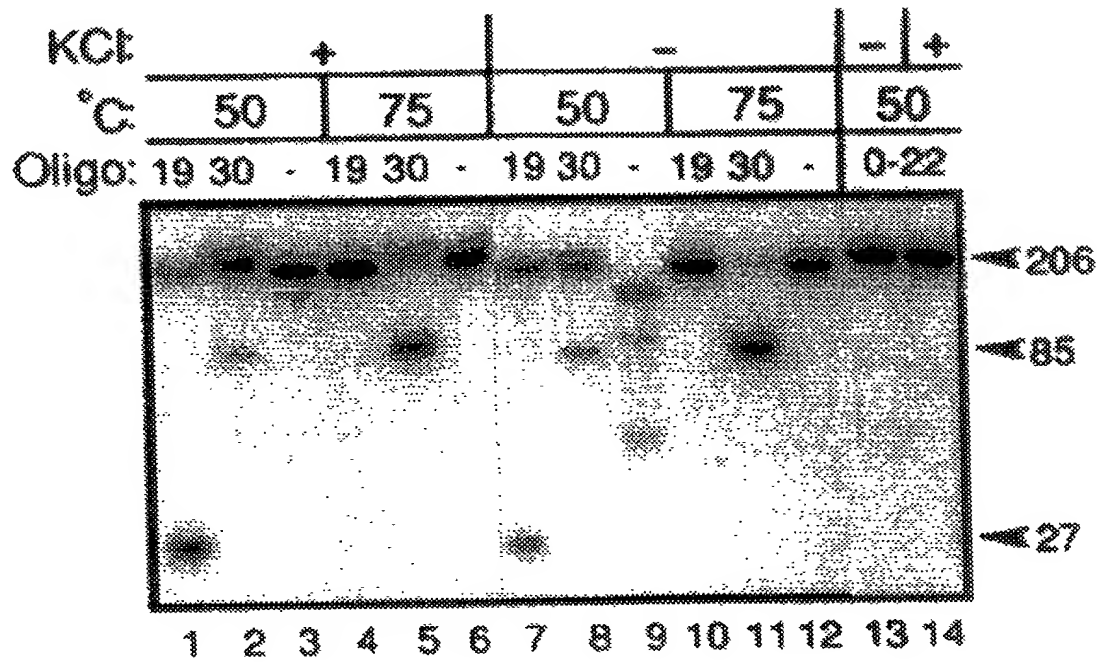


FIG. 12B

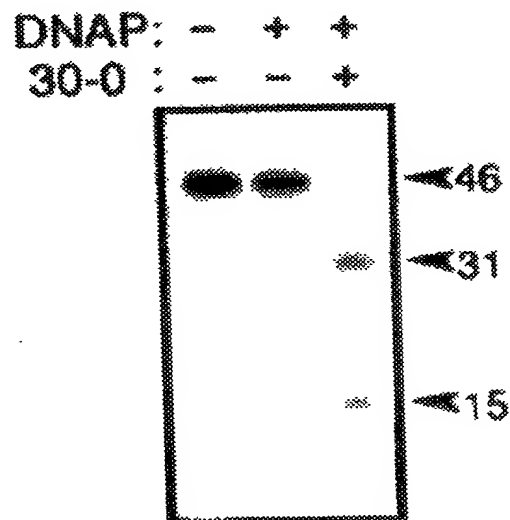


FIG. 13B

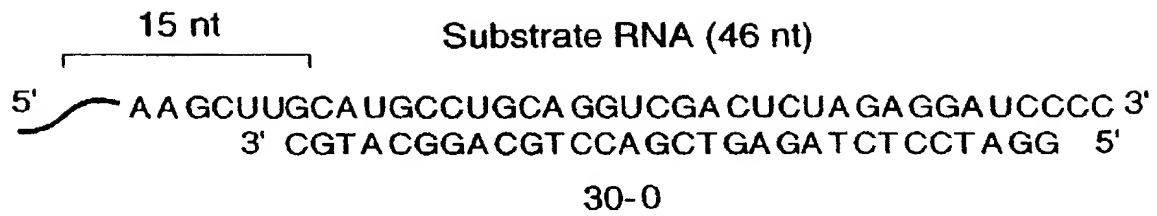


FIG. 13A

-35
 TTGACAAATTAATCATCGGCTCGTATAATGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCG
 -10
 RBS
 MetAsnSer...
 ATGAATTCGAGCTCGGTACCCGGGATCCTCTAGAGTCGACCTGCAGGCATGCAAGCTTGGCACTGGCC
 EcoRI KpnI BamHI SmaI SstI XbaI Sall PstI SphI HindIII

FIG. 14B

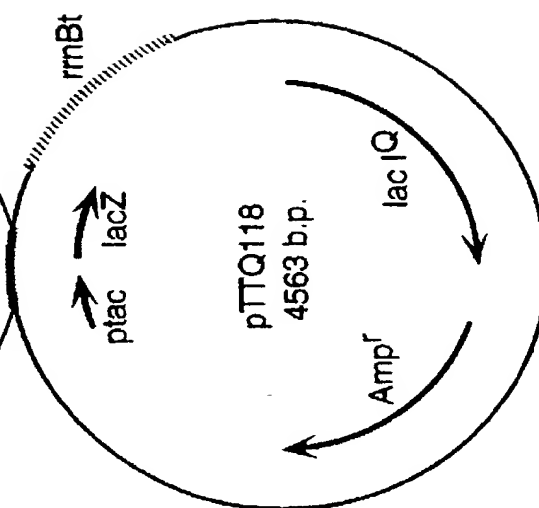
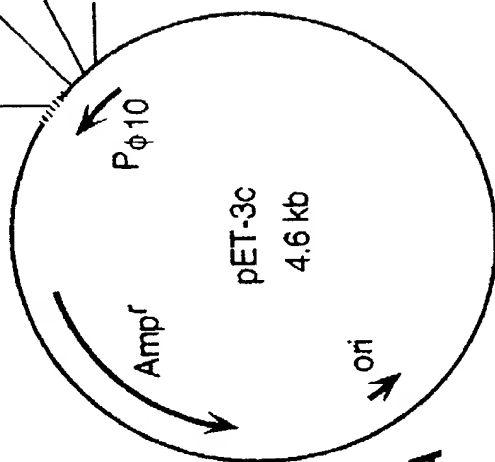
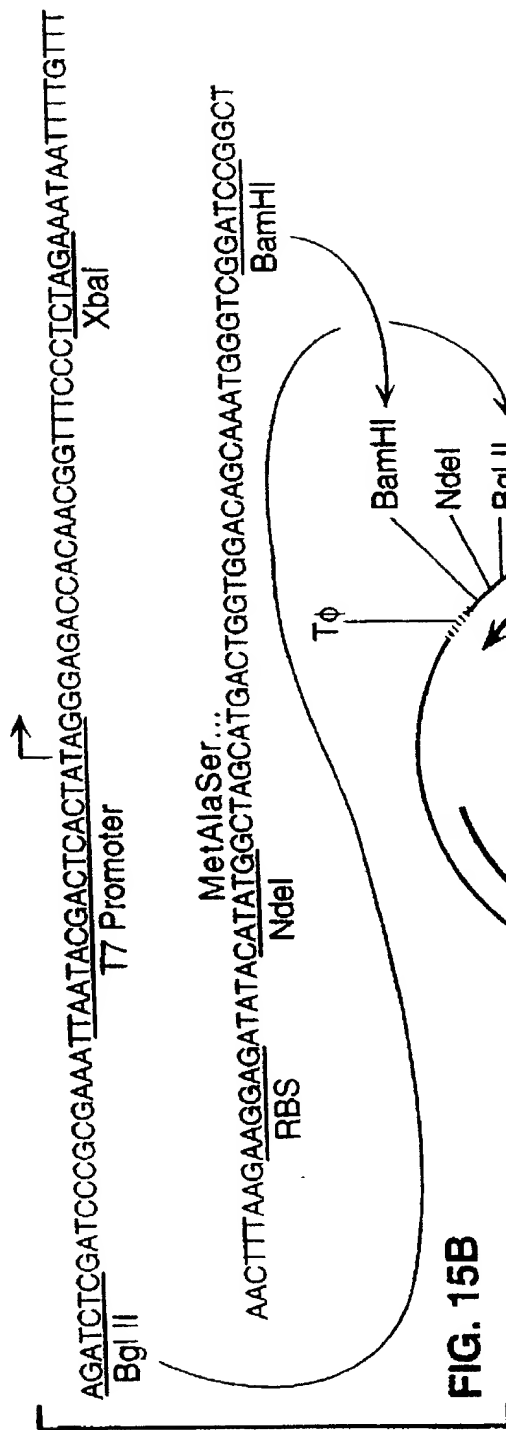


FIG. 14A

RBS: Ribosome binding site
ptac: Synthetic tac promoter
lac I^Q: Lac repressor gene
lacZ: Beta-galactosidase alpha fragment
rmBt: E. coli rmB transcription terminator

FIG. 14C



$P_{\phi 10}$: Bacteriophage T7 $\phi 10$ promoter
 T_{ϕ} : T7 ϕ Terminator
 RBS: Ribosome binding site

FIG. 15C

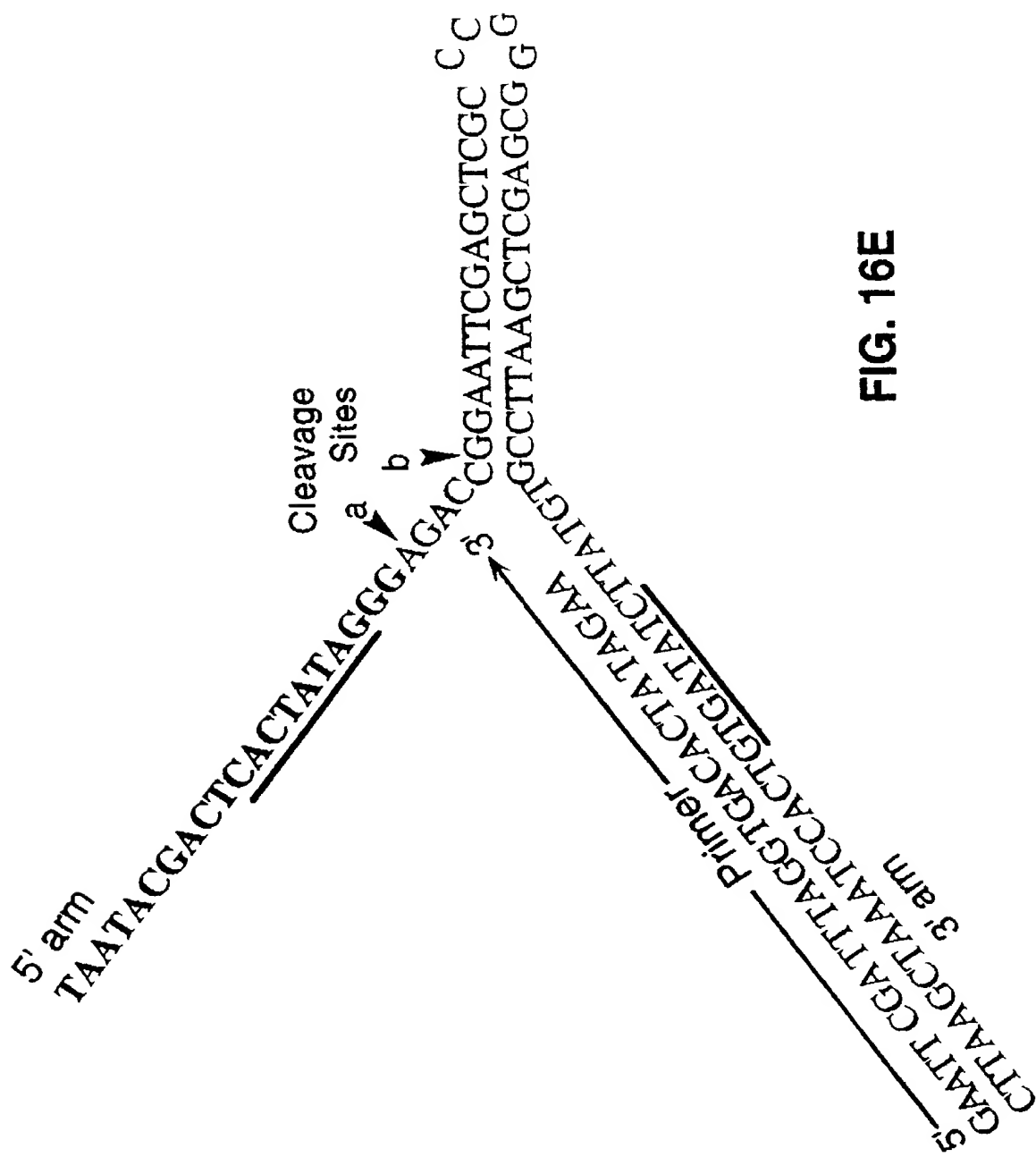


FIG. 16E

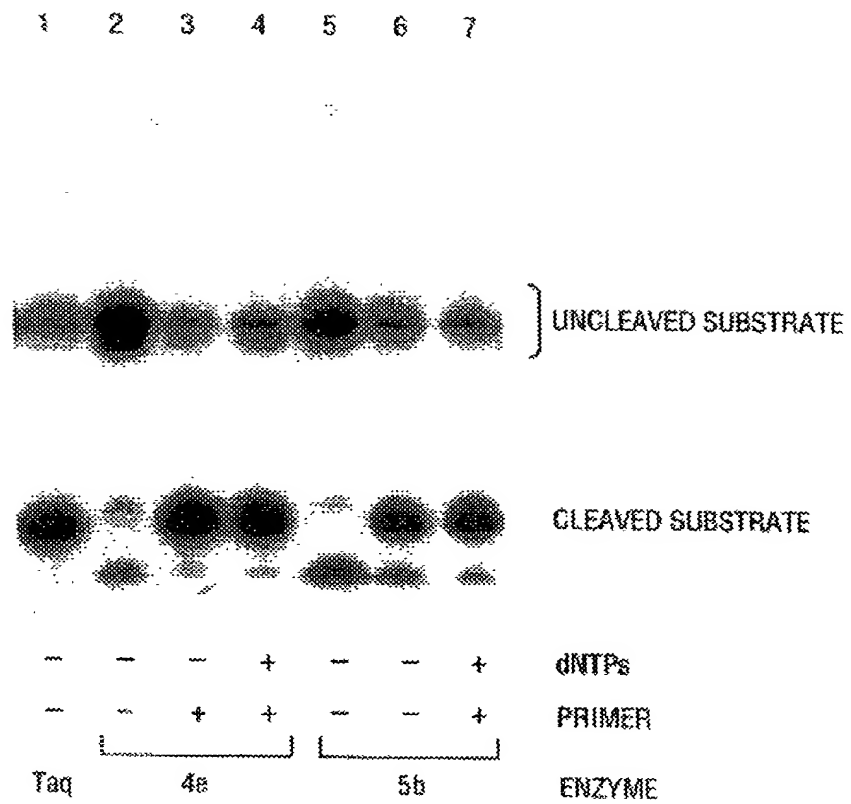


FIG. 17

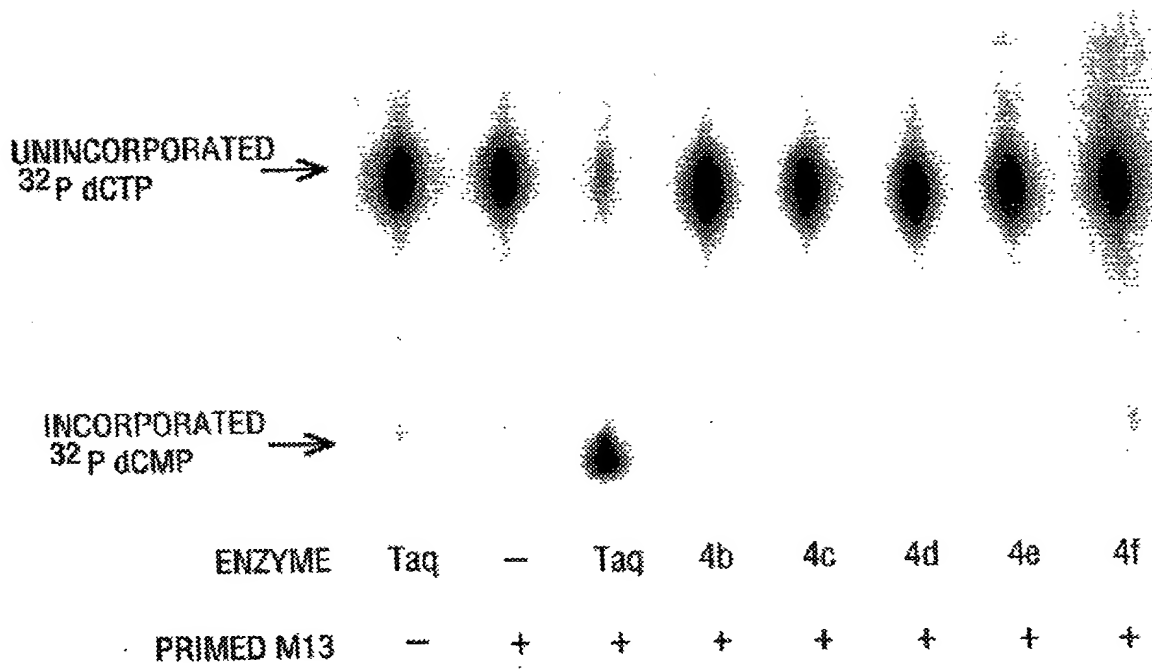


FIG. 18

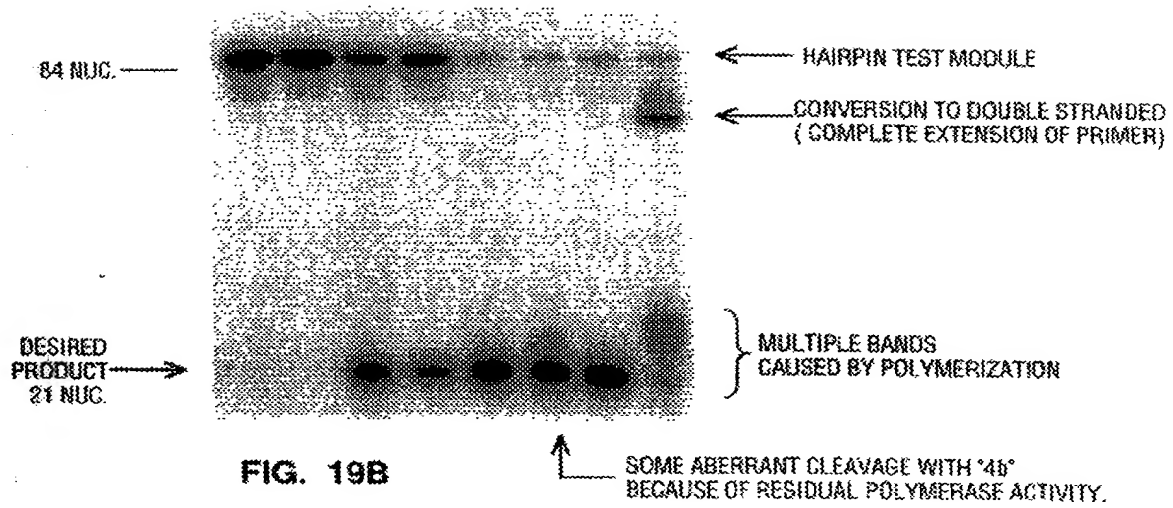
(³²P) 5' TAATACGACTCACTATAGGGAGAC CGGAAT T C

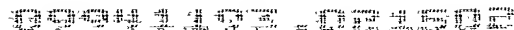
Sites of Cleavage with a gap of 6 nt.

60% 40%

5' 3' GATTTAGGTGACACTATAG CTTAAGCTAAATCCACTGTGATATCTTATGTGCCTTA A G

FIG. 19A





Sequence of alpha primer:
5' GACGAACAAGCGAGACAGCG 3'

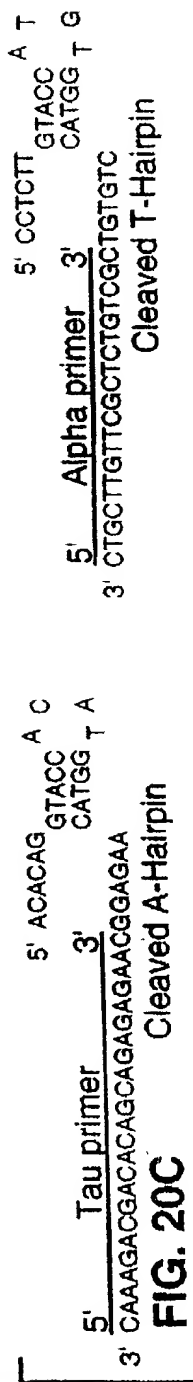


FIG. 20D

5' GTTCTGCTGTGCTCTCTTTGGCTCTTTGACCATGTGGTACCTGTGTGCTGTCTCGCTTTCGTC 3'

3' CAAAGACGACACAGCAGAGAGACGGAGAACATGTTACCATGGACACAGCGACAGAGCGAACAAGCAGGC 5'

Restriction sites indicated: BsmAI, NlaIII, HgiCI, MnlI, RsaI/NlaIV, RsaI, KpnI, BsmAI, T-Hairpin, A-Hairpin.

FIG. 20D

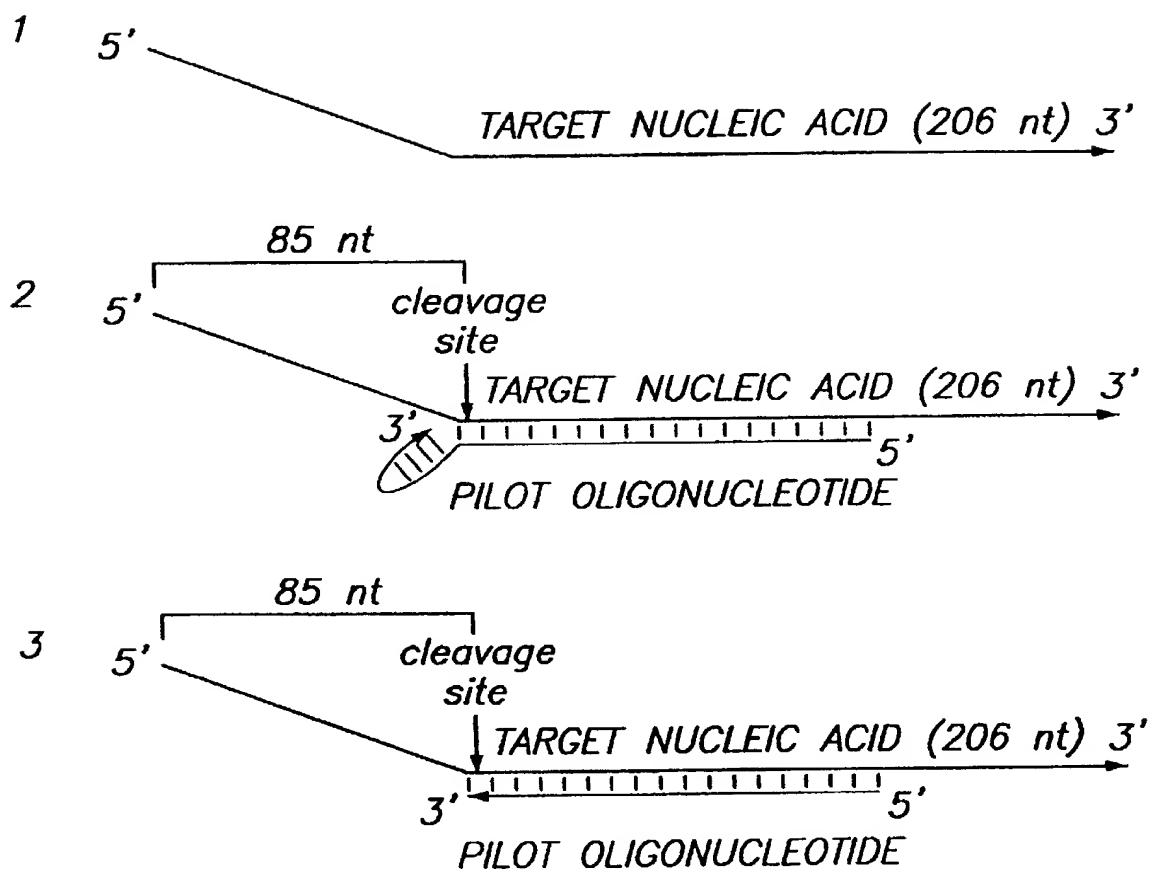


FIG. 22A

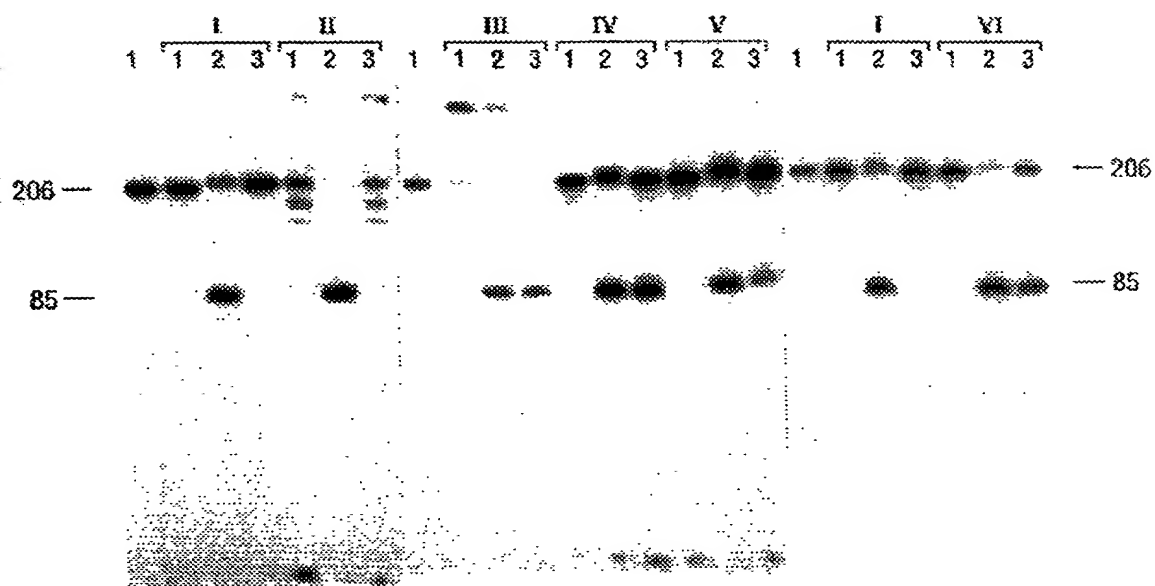


FIG. 22B

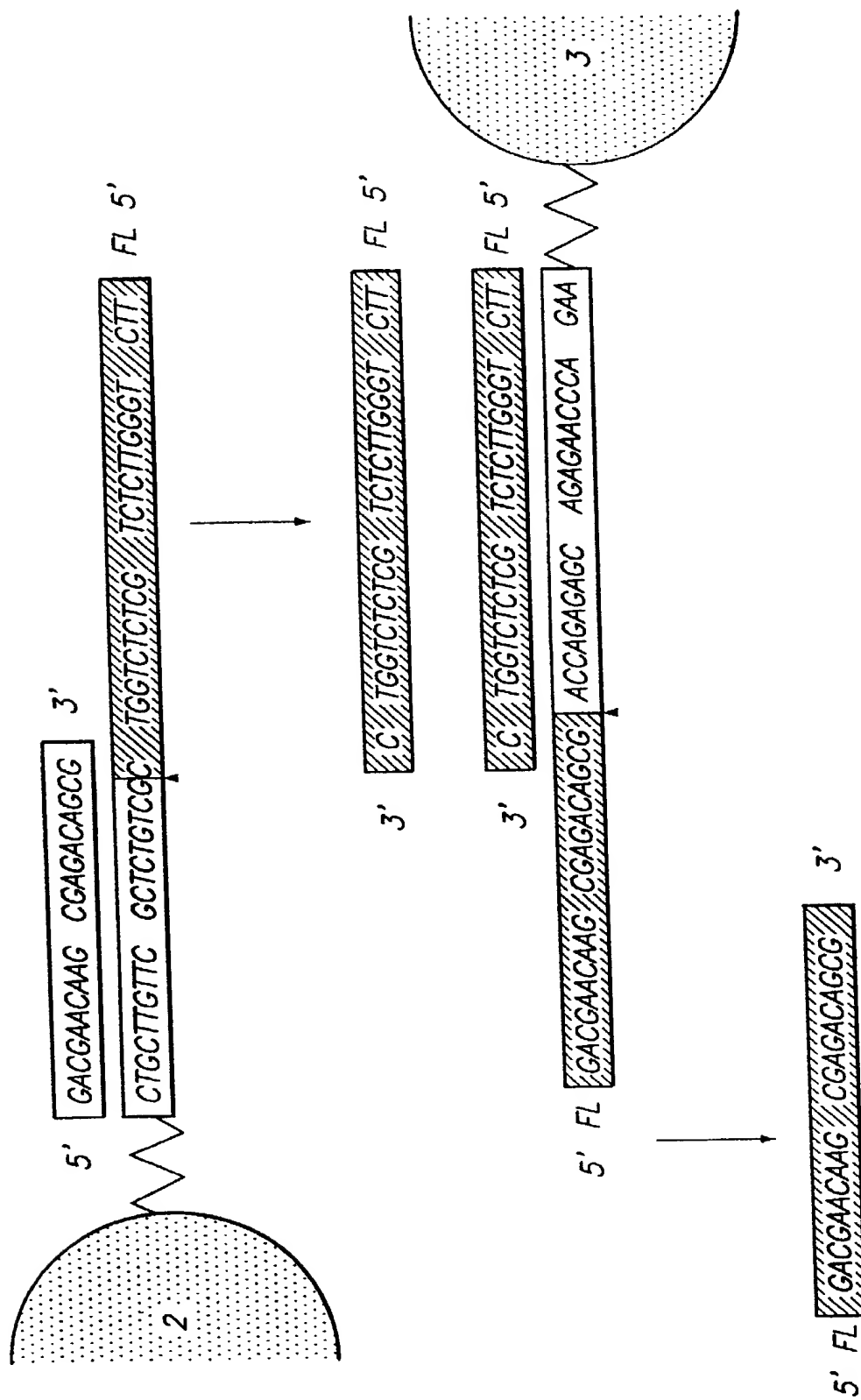


FIG. 23

!



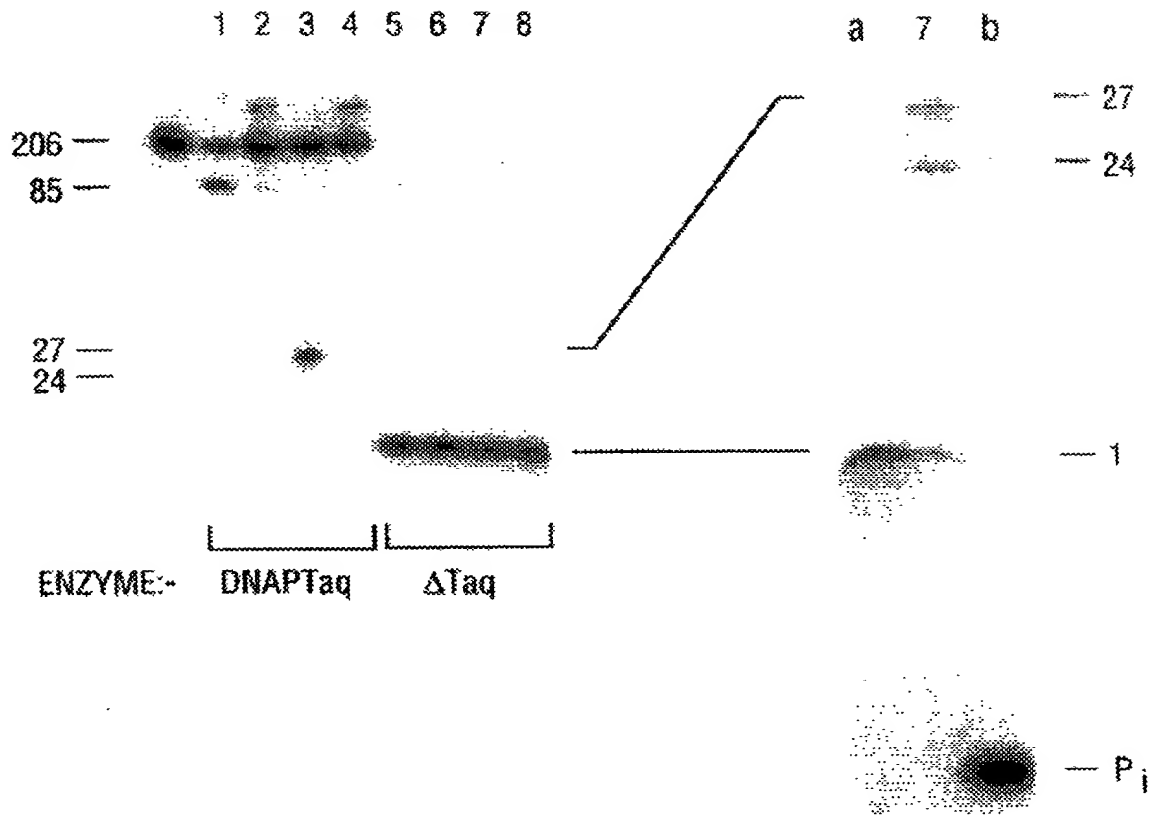


FIG. 25A

FIG. 25B

FIG. 26A

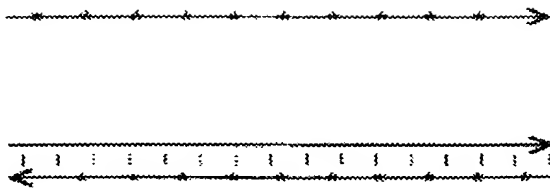
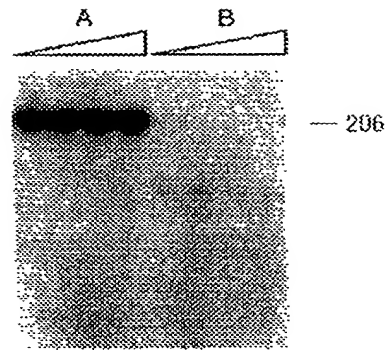


FIG. 26B

$\leftarrow \approx 3\frac{1}{2}p$



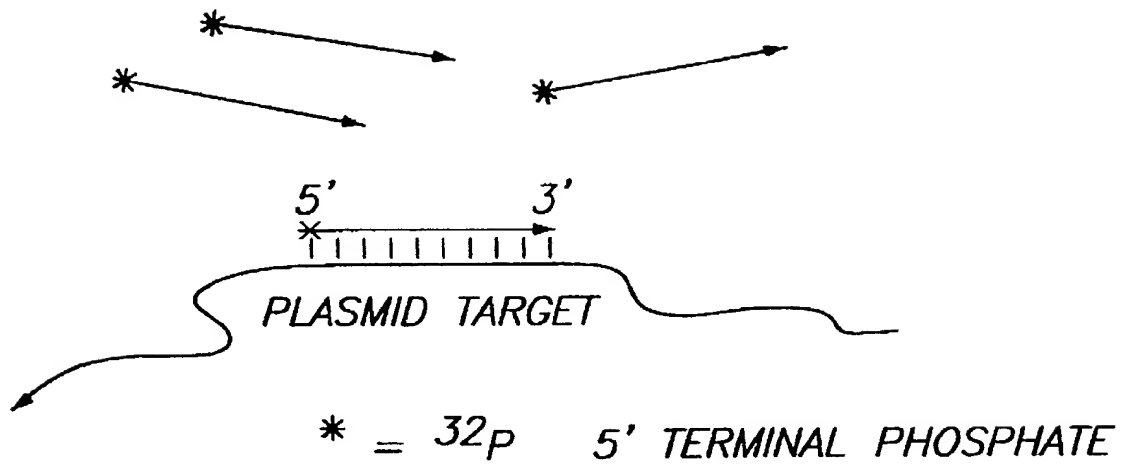


FIG. 28A

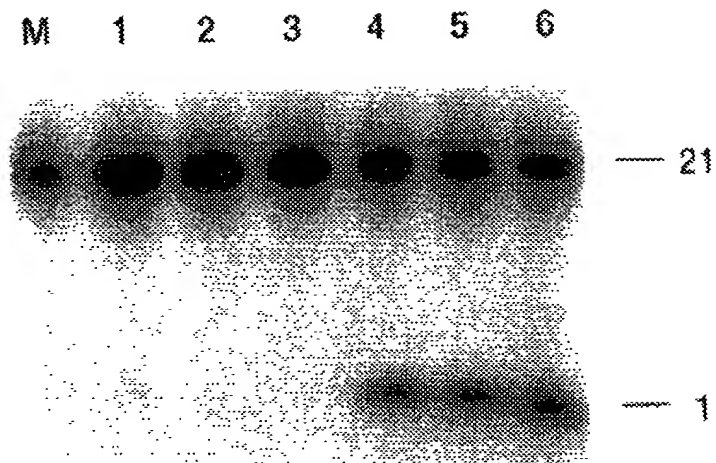


FIG. 28B

FIG. 29

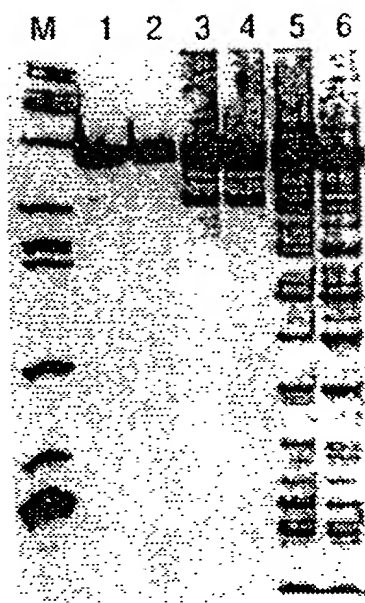


FIG. 30

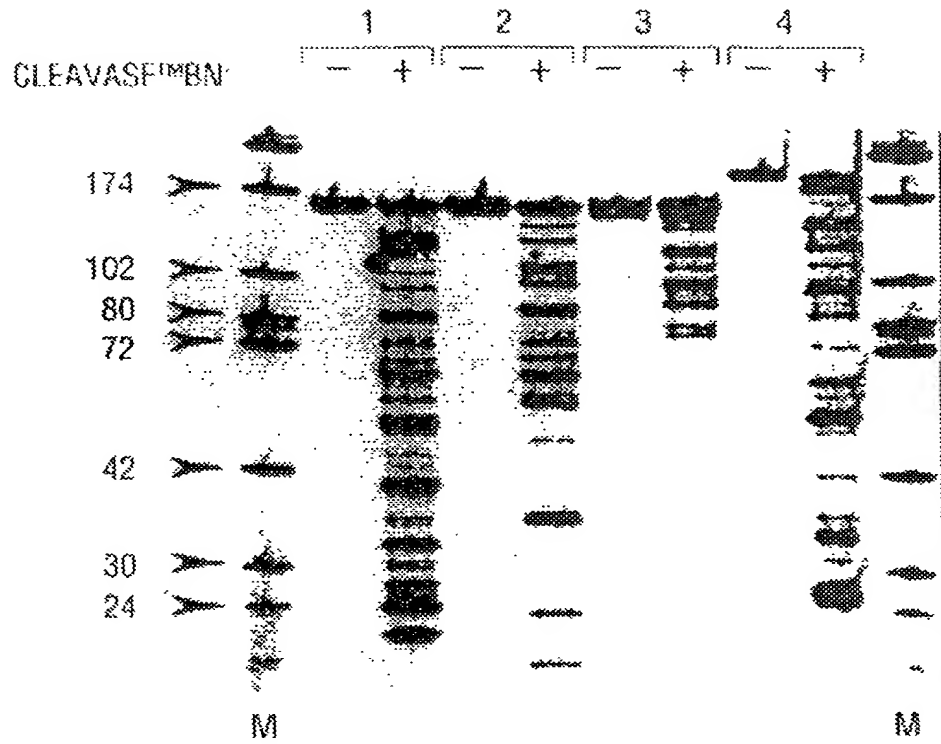


FIG. 31

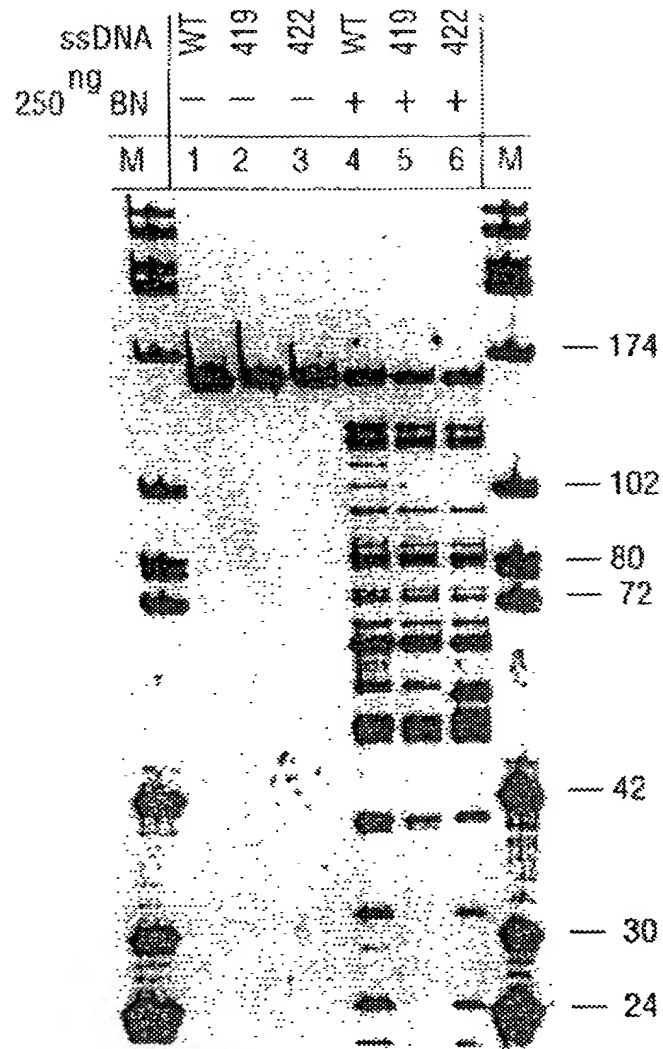


FIG. 32

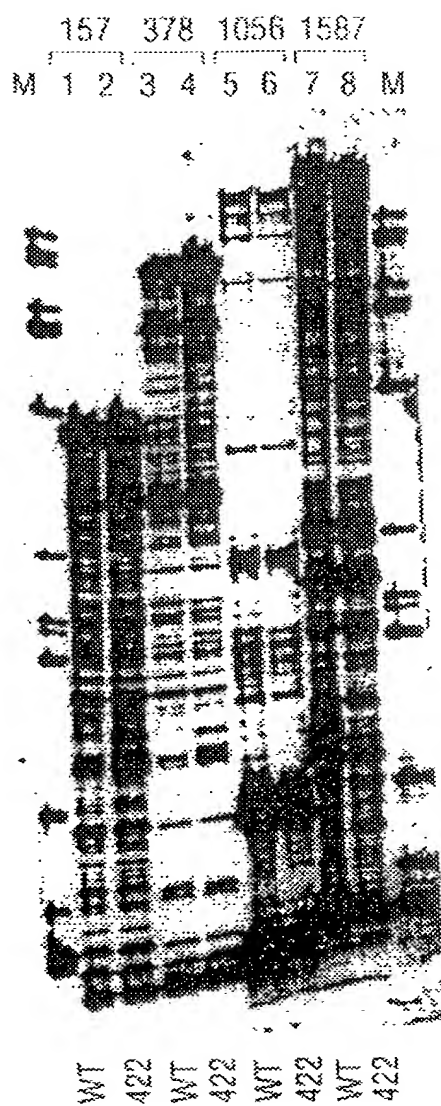


FIG. 33

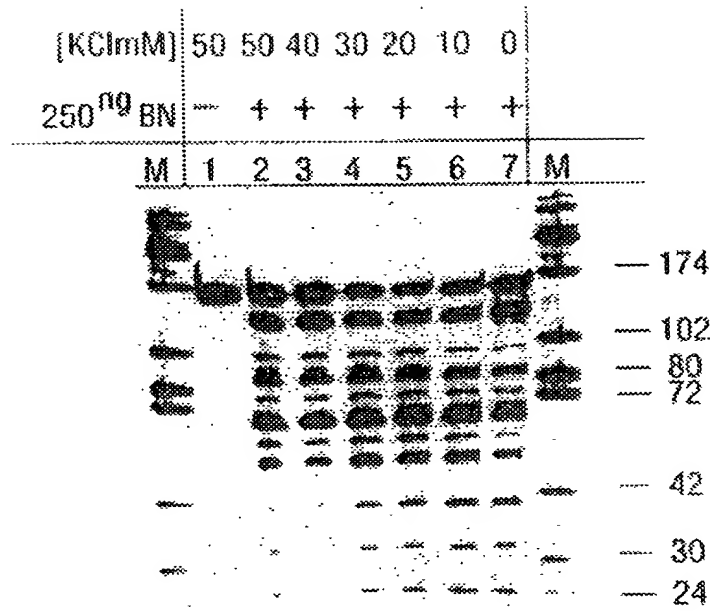


FIG. 35

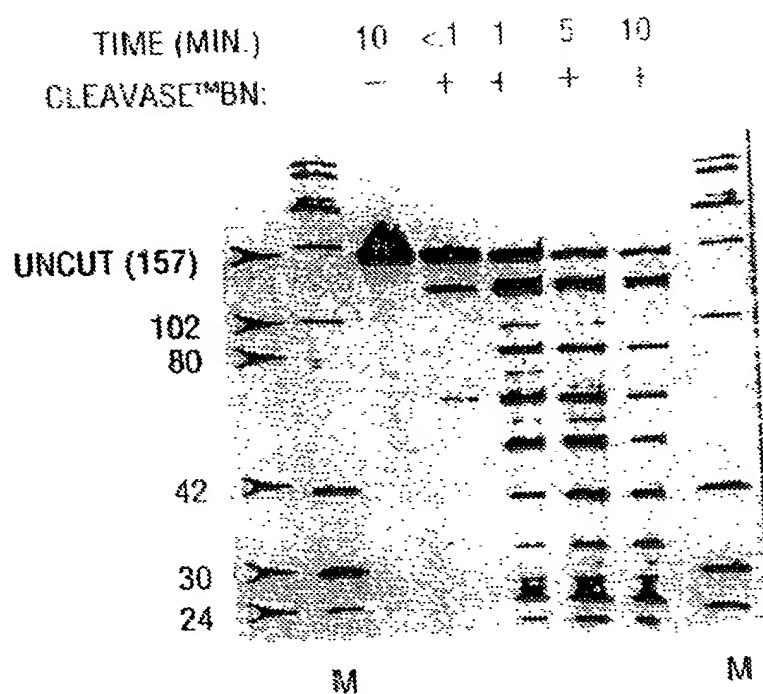


FIG. 36

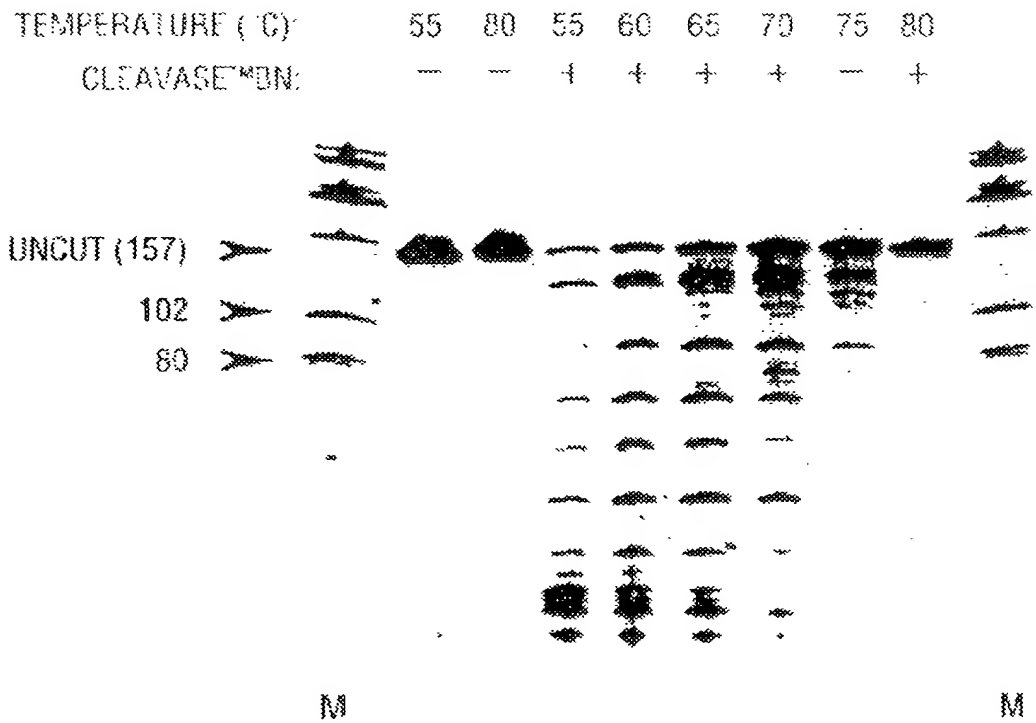


FIG. 37

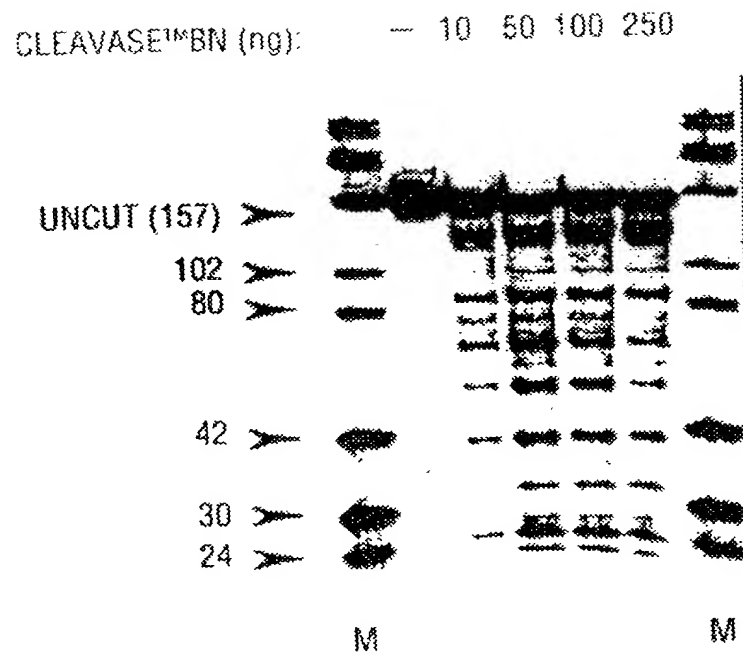


FIG. 38

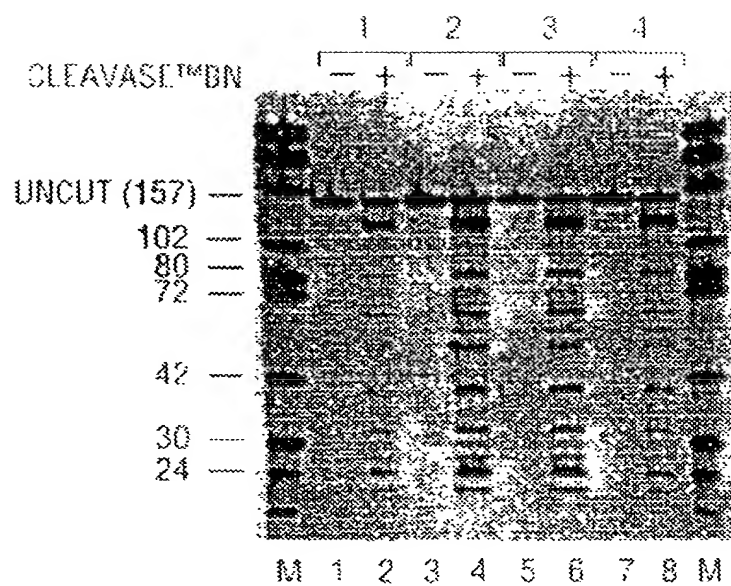


FIG. 39

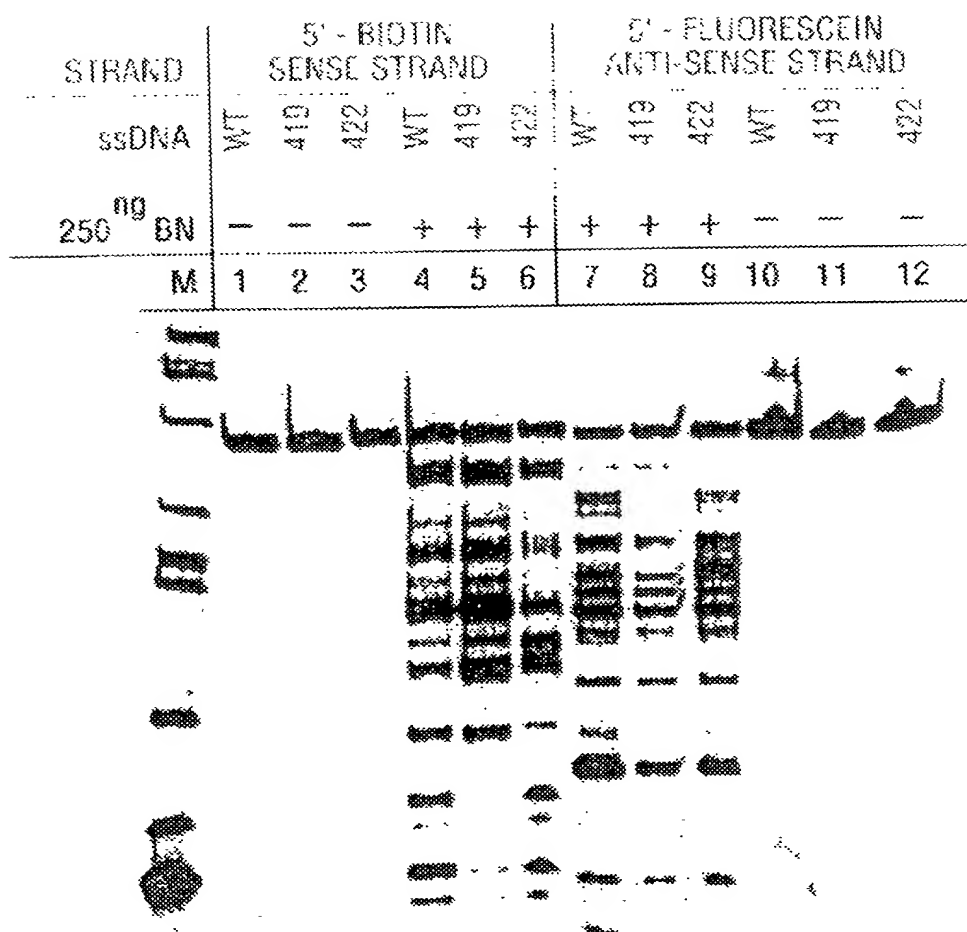


FIG. 40

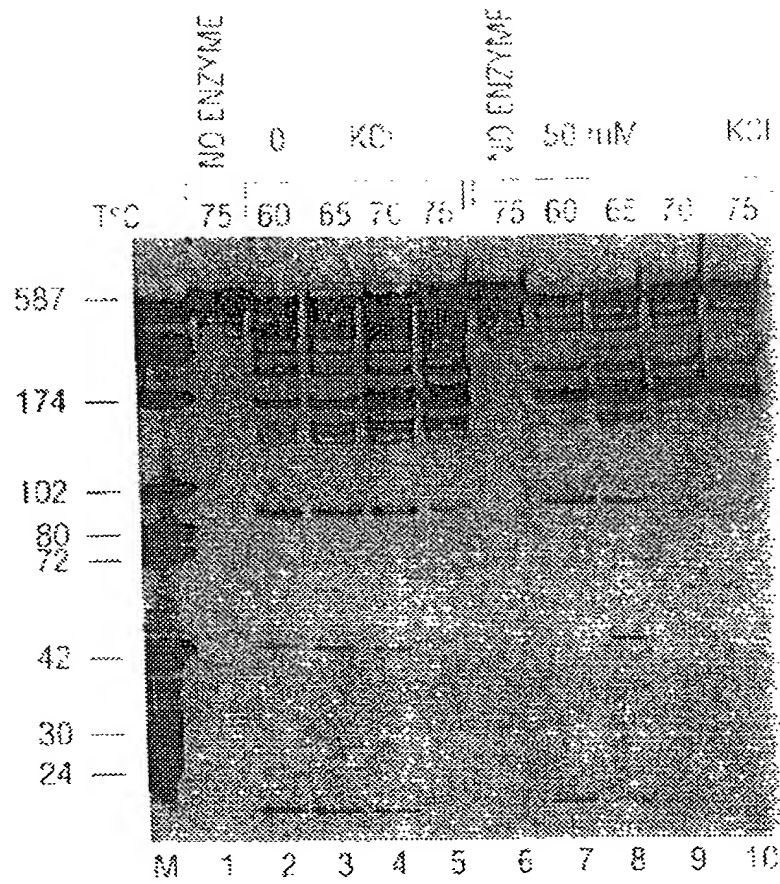


FIG. 41

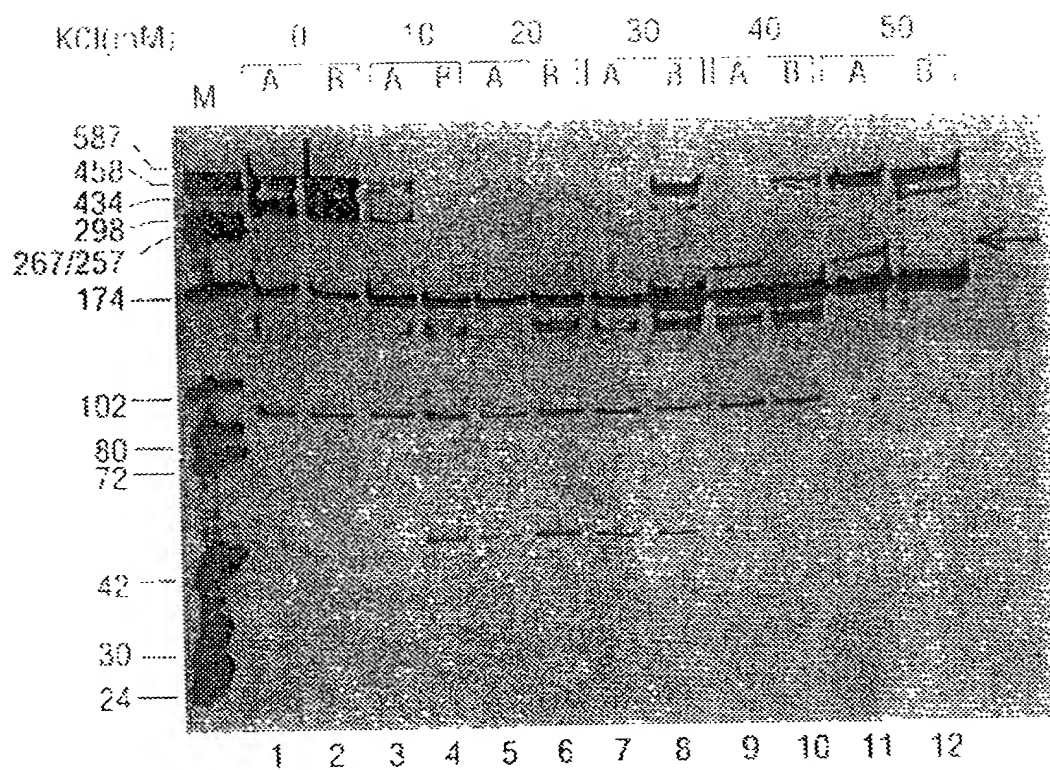


FIG. 42

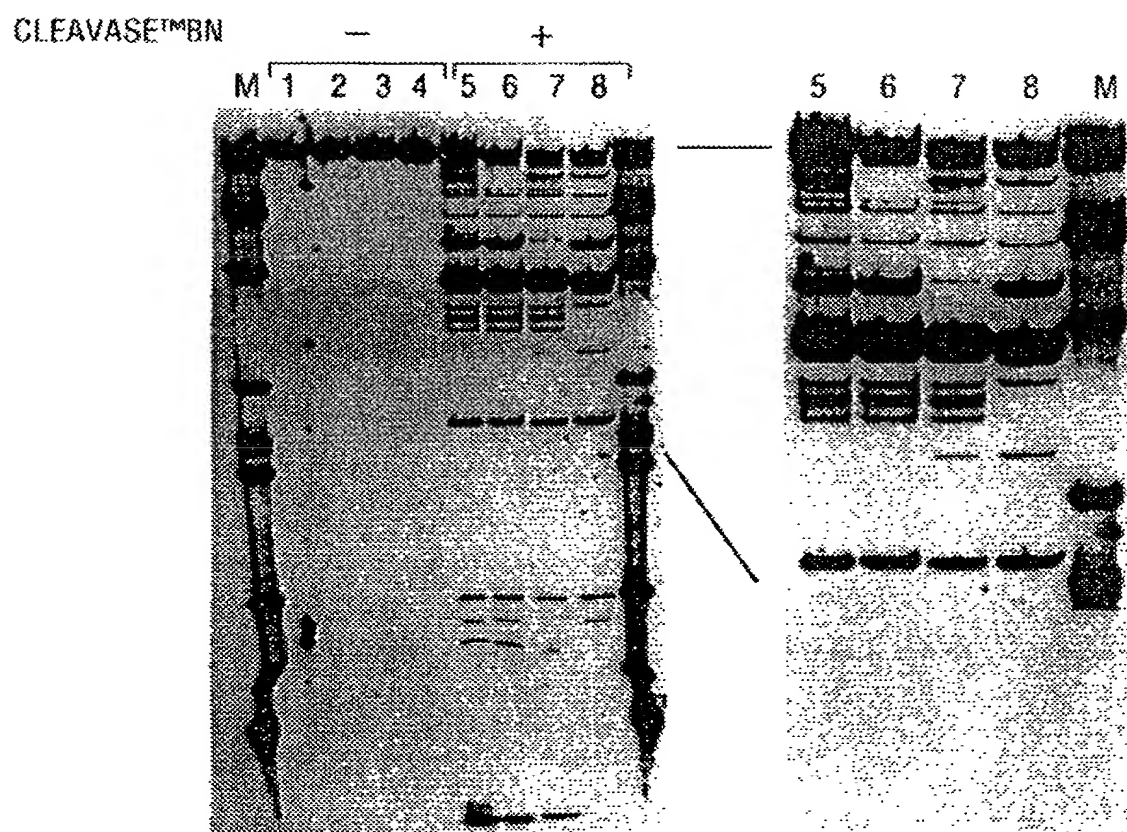


FIG. 43

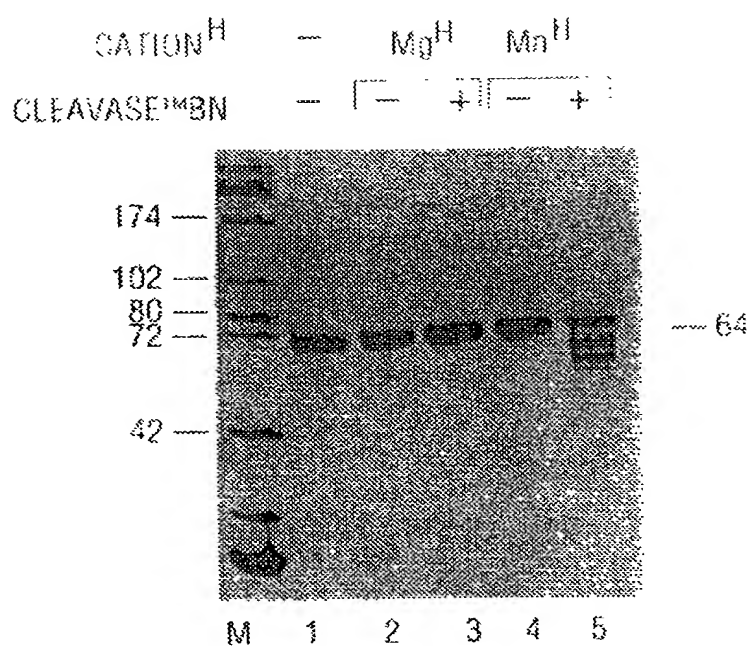


FIG. 44

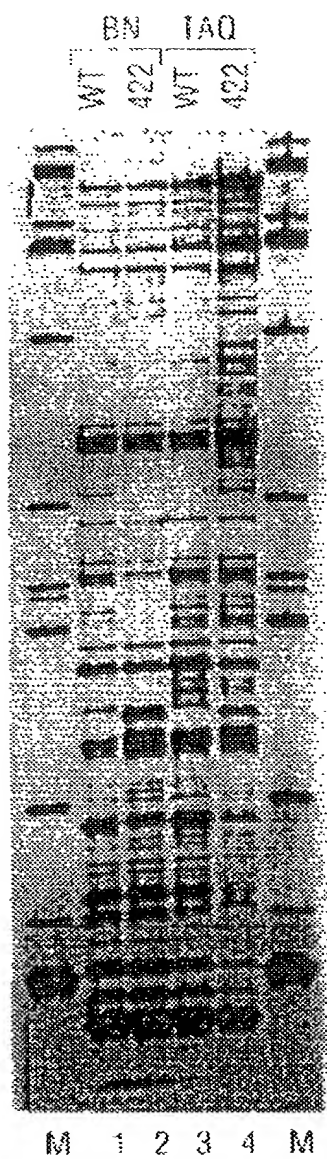


FIG. 45

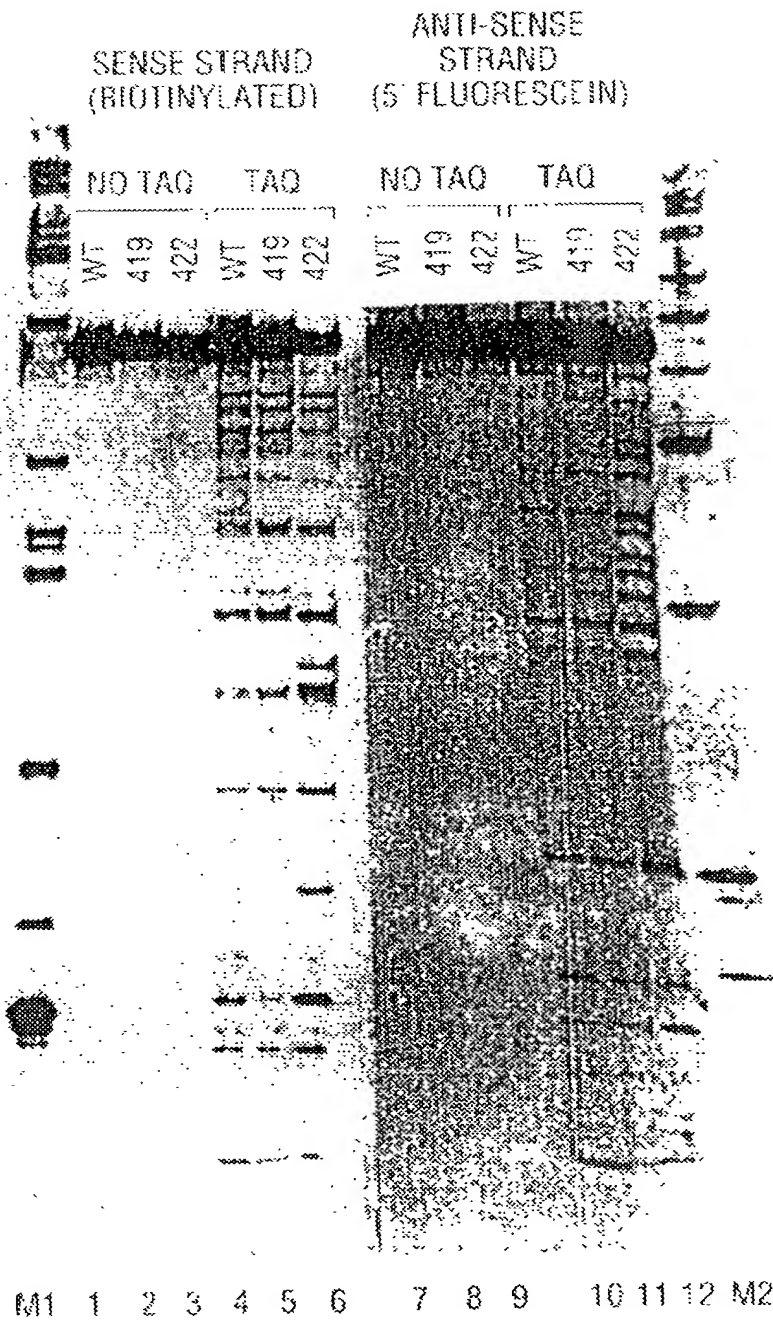


FIG. 46

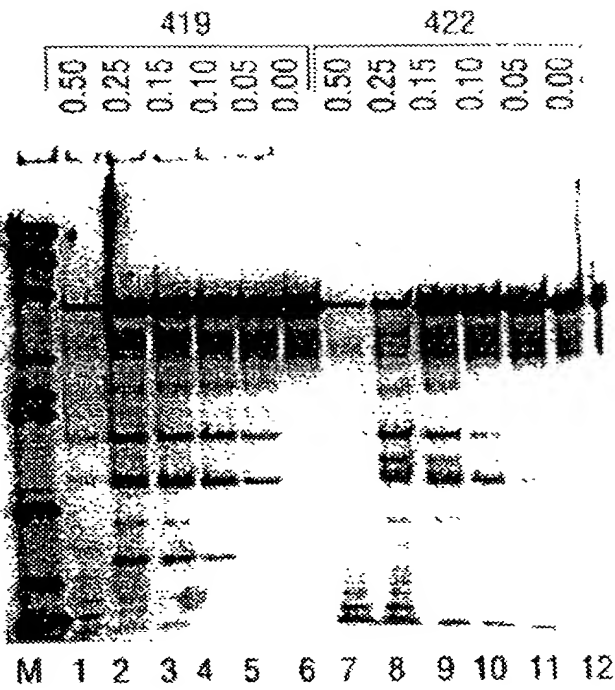


FIG. 47

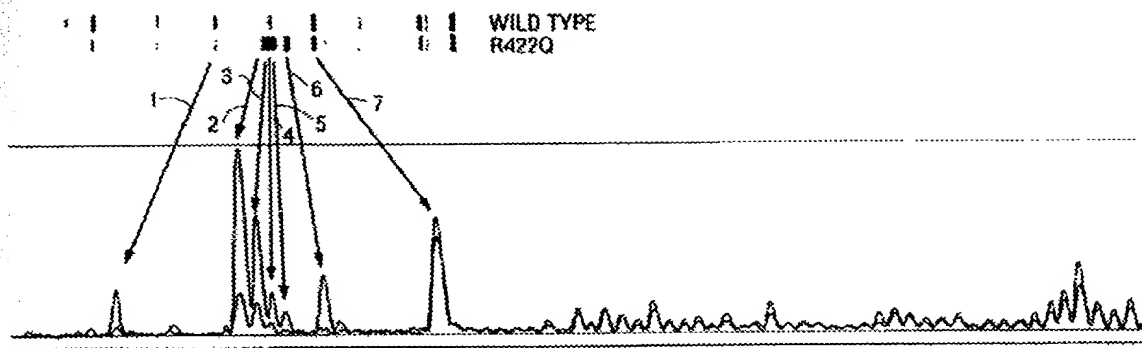


FIG. 48

L.100.8-1 5'GGCTGACAAGAAGGAAACTCGCTGAGACAGCAGGGACTTTCCACAAGGGG
(SEQ ID NO: 76) 3'CCGACTGTTCTTCCTTGAGCGACTCTGTCGTCCCTGAAAGGTGTTCCCC

L.46.16-10 5'GGCTGACAAGAAGGAAACTCGCTGAGATAGCAGGGACTTTCCACAAGGGG
(SEQ ID NO: 77) 3'CCGACTGTTCTTCCTTGAGCGACTCTATCGTCCCTGAAAGGTGTTCCCC

L.46.16-12 5'GGCTGACAAGAAGGAAACTCGCTGAGATAGCAGGGACTTTCCACAAGGGG
(SEQ ID NO: 78) 3'CCGACTGTTCTTCCTTGAGCGACTCTATCGTCCCTGAAAGGTGTTCCCC

L19.16-3 5'GGCTGACAAGAAGGAAACTCGCTGAGACAGCAGGGACTTTCCACAAGGGG
(SEQ ID NO: 79) 3'CCGACTGTTCTTCCTTGAGCGACTCTGTCGTCCCTGAAAGGTGTTCCCC

L.CEM/251 5'GGCTGACAAGAAGGAAACTCGCTGAAACAGCAGGGACTTTCCACAAGGGG
(SEQ ID NO: 80) 3'CCGACTGTTCTTCCTTGAGCGACTTTGTCGTCCCTGAAAGGTGTTCCCC

L.36.8-3 5'GGCTGACAAGAAGGAAACTCGCTGAGACAGCAGGGACTTTCCACAAGGGG
(SEQ ID NO: 81) 3'CCGACTGTTCTTCCTTGAGCGACTCTGTCGTCCCTGAAAGGTGTTCCCC

FIG. 49A

CGCGCTGTTCTTCCTTGAGCGACTCTGTCGTCCCTGAAAGGTGTTCCCC

L.100.8-1	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC	200
L.46.16-10	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC	
L.46.16-12	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC	
L.19.16-3	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC	
L.CEM/251	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC	
L.36.8-3	GAGGCTGGCAGATTGAGCCCTAGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGATCCTCCAAGAGAGGTCGTGATCGTCCATC	

FIG. 49D

200 199 198 197 196 195 194 193 192 191 190 189 188 187 186 185 184 183 182 181 180 179 178 177 176 175 174 173 172 171 170 169 168 167 166 165 164 163 162 161 160 159 158 157 156 155 154 153 152 151 150 149 148 147 146 145 144 143 142 141 140 139 138 137 136 135 134 133 132 131 130 129 128 127 126 125 124 123 122 121 120 119 118 117 116 115 114 113 112 111 110 109 108 107 106 105 104 103 102 101 100 99 98 97 96 95 94 93 92 91 90 89 88 87 86 85 84 83 82 81 80 79 78 77 76 75 74 73 72 71 70 69 68 67 66 65 64 63 62 61 60 59 58 57 56 55 54 53 52 51 50 49 48 47 46 45 44 43 42 41 40 39 38 37 36 35 34 33 32 31 30 29 28 27 26 25 24 23 22 21 20 19 18 17 16 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1

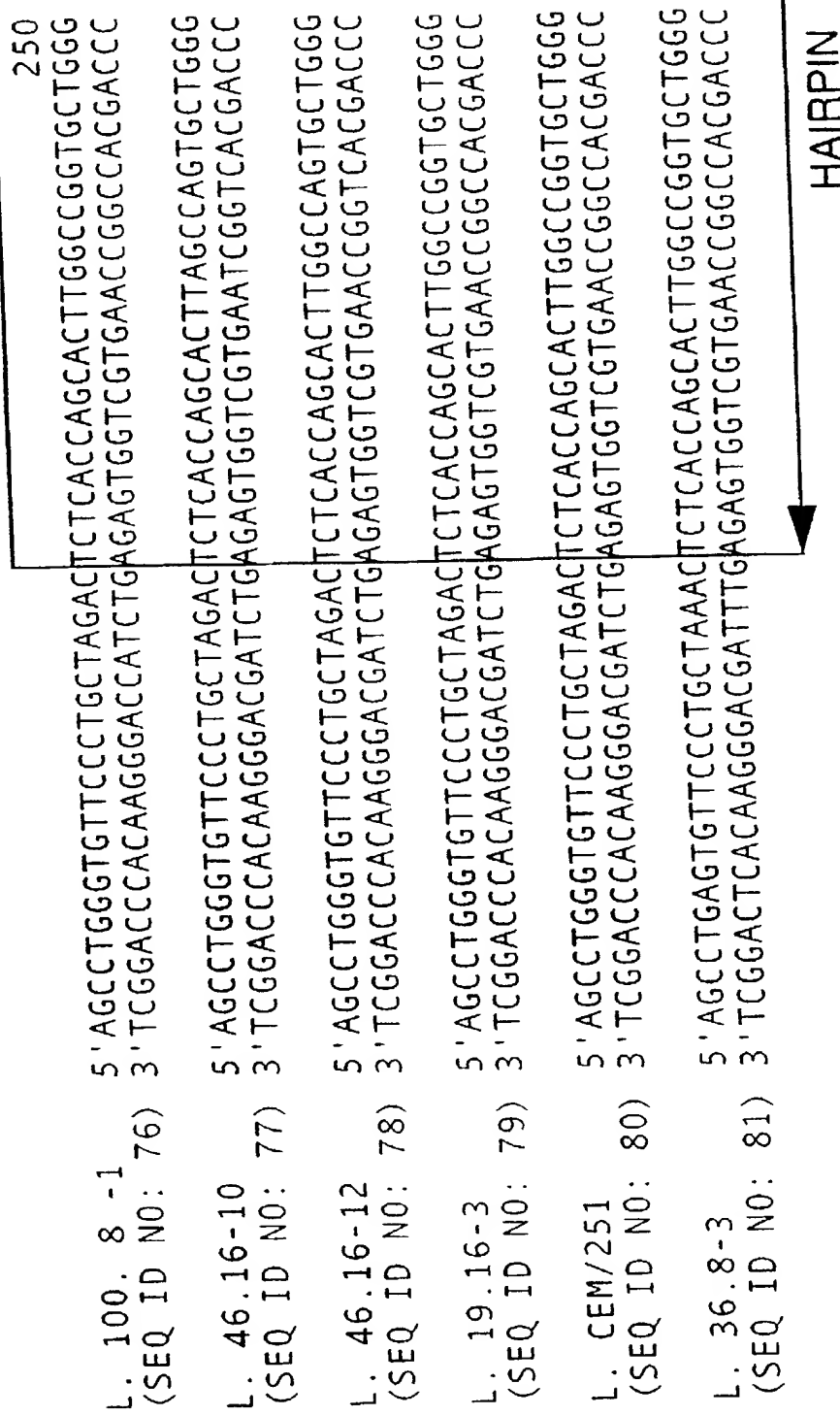


FIG. 49E

250 250 250 250 250 250

L.100.8-1	<div>350</div> <div>5'ATTTTGAAGTAGGCCAGTGTGTGTTCCCATCTCTCCTAGCCGCCGCCCTG G 3'</div> <div>3'TAAATCTTCATCCGGTCACACACAAGGGTAGAGAGGATCGGCGGCGGAC C 5'</div>
L.46.16-10	<div>5'ATTTTGAAGTAAGCCAGTGTGTGTTCCCATCTCTCCTAGCCGCCGCCCTG G 3'</div> <div>3'TAAATCTTCATTCGGTCACACACAAGGGTAGAGAGGATCGGCGGCGGAC C 5'</div>
L.46.16-12	<div>5'ATTTTGAAGTAAGCCAGTGTGTGTTCCCATCTCTCCTAGCCGCCGCCCTG G 3'</div> <div>3'TAAATCTTCATTCGGTCACACACAAGGGTAGAGAGGATCGGCGGCGGAC C 5'</div>
L.19.16-3	<div>5'ATTTTGAAGTAGGCTAGTGTGTGTTCCCATCTCTCCTAGCCGCCGCCCTG G 3'</div> <div>3'TAAATCTTCATCCGATCACACACAAGGGTAGAGAGGATCGGCGGCGGAC C 5'</div>
L.CEM/251	<div>5'ATTTTGAAGTAAGCTAGTGTGTGTTCCCATCTCTCCTAGCCGCCGCCCTG G 3'</div> <div>3'TAAATCTTCATTCGATCACACACAAGGGTAGAGAGGATCGGCGGCGGAC C 5'</div>
L.36.8-3	<div>5'ATTTTGAAGTAGGCTAGTGTGTGTTCCCATCTCTCCTAGCCGCCGCCCTG G 3'</div> <div>3'TAAATCTTCATCCGATCACACACAAGGGTAGAGAGGATCGGCGGCGGAC C 5'</div>

FIG. 49G

350 349 348 347 346 345 344 343 342 341 340 339 338 337 336 335 334 333 332 331 330 329 328 327 326 325 324 323 322 321 320 319 318 317 316 315 314 313 312 311 310 309 308 307 306 305 304 303 302 301 300 299 298 297 296 295 294 293 292 291 290 289 288 287 286 285 284 283 282 281 280 279 278 277 276 275 274 273 272 271 270 269 268 267 266 265 264 263 262 261 260 259 258 257 256 255 254 253 252 251 250 249 248 247 246 245 244 243 242 241 240 239 238 237 236 235 234 233 232 231 230 229 228 227 226 225 224 223 222 221 220 219 218 217 216 215 214 213 212 211 210 209 208 207 206 205 204 203 202 201 200 199 198 197 196 195 194 193 192 191 190 189 188 187 186 185 184 183 182 181 180 179 178 177 176 175 174 173 172 171 170 169 168 167 166 165 164 163 162 161 160 159 158 157 156 155 154 153 152 151 150 149 148 147 146 145 144 143 142 141 140 139 138 137 136 135 134 133 132 131 130 129 128 127 126 125 124 123 122 121 120 119 118 117 116 115 114 113 112 111 110 109 108 107 106 105 104 103 102 101 100 99 98 97 96 95 94 93 92 91 90 89 88 87 86 85 84 83 82 81 80 79 78 77 76 75 74 73 72 71 70 69 68 67 66 65 64 63 62 61 60 59 58 57 56 55 54 53 52 51 50 49 48 47 46 45 44 43 42 41 40 39 38 37 36 35 34 33 32 31 30 29 28 27 26 25 24 23 22 21 20 19 18 17 16 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1

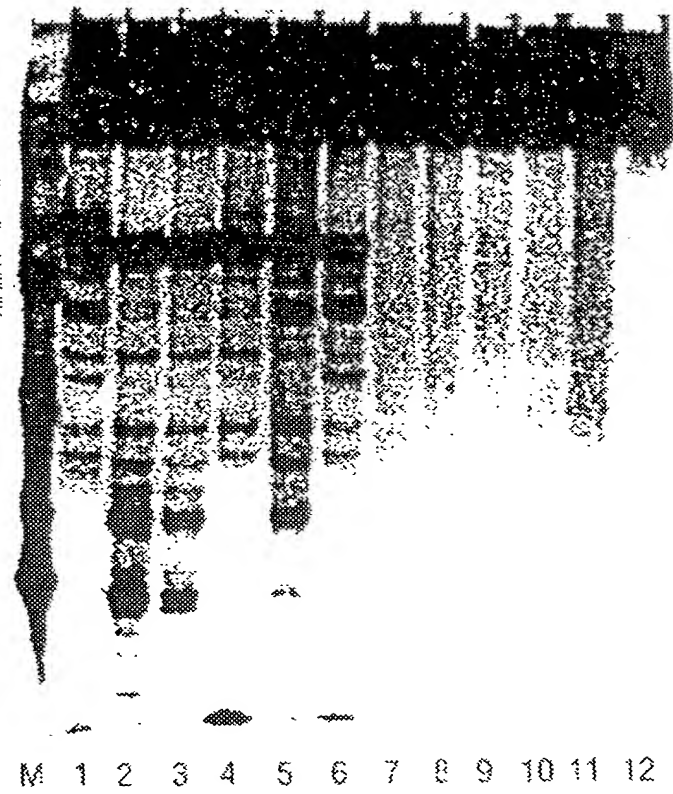


FIG. 50

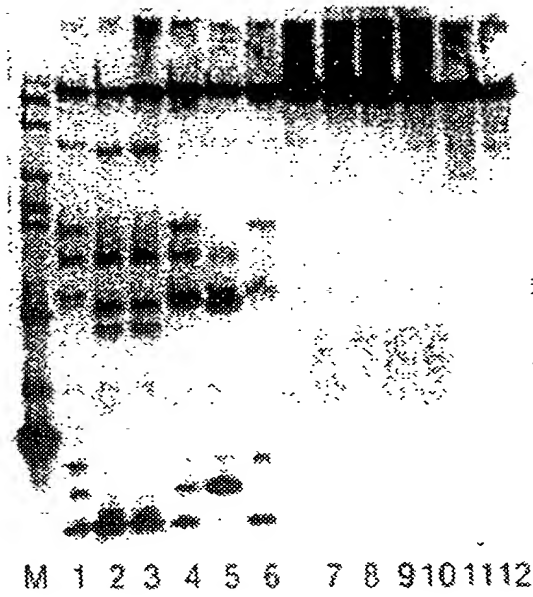


FIG. 51

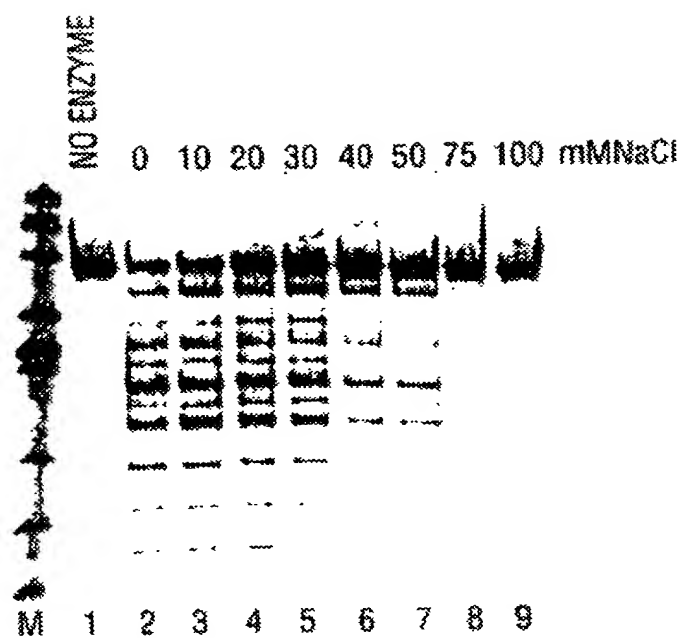


FIG. 52

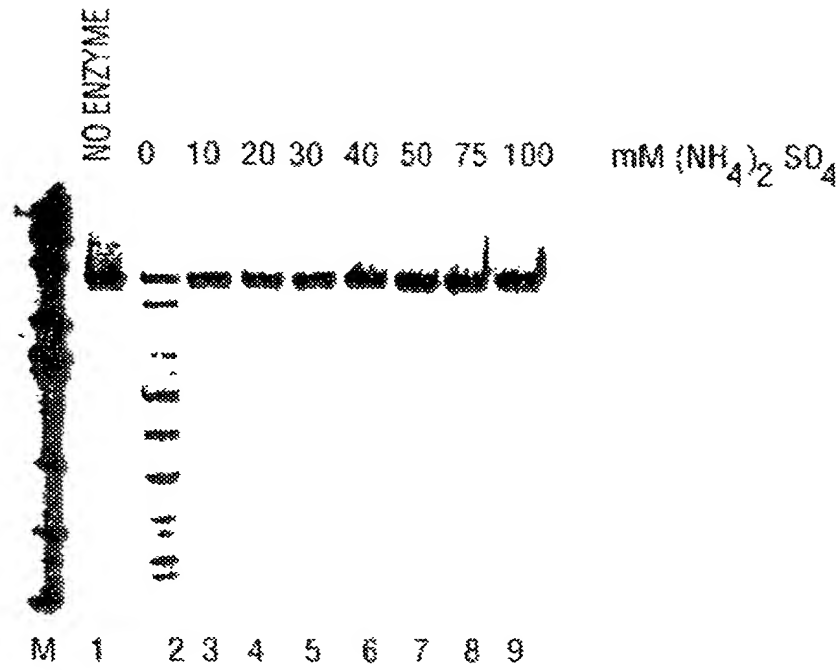


FIG. 53

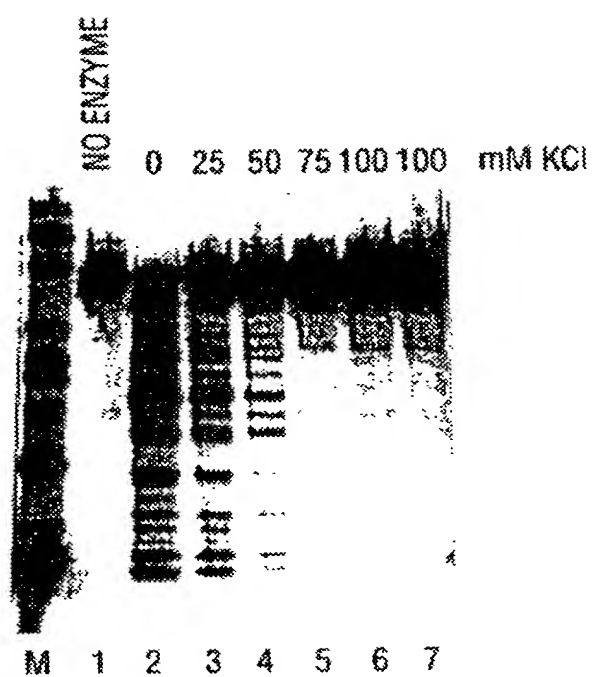


FIG. 54

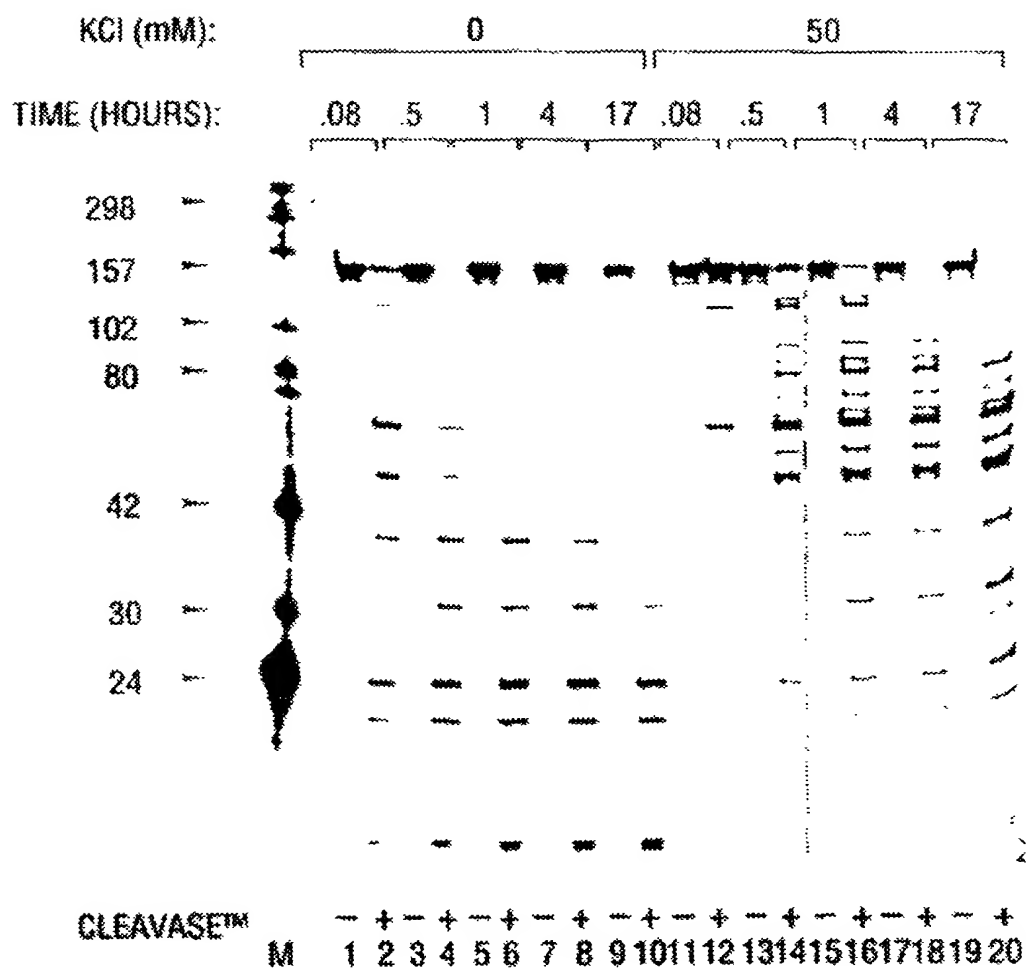


FIG. 55

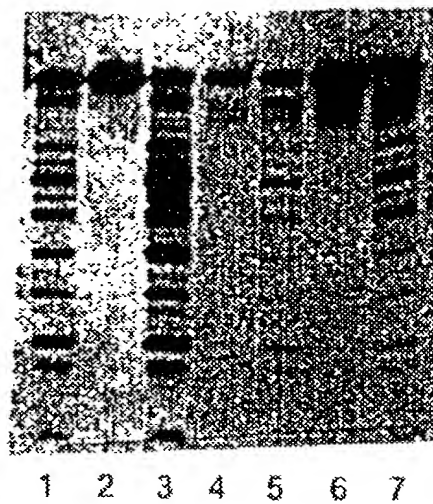


FIG. 56

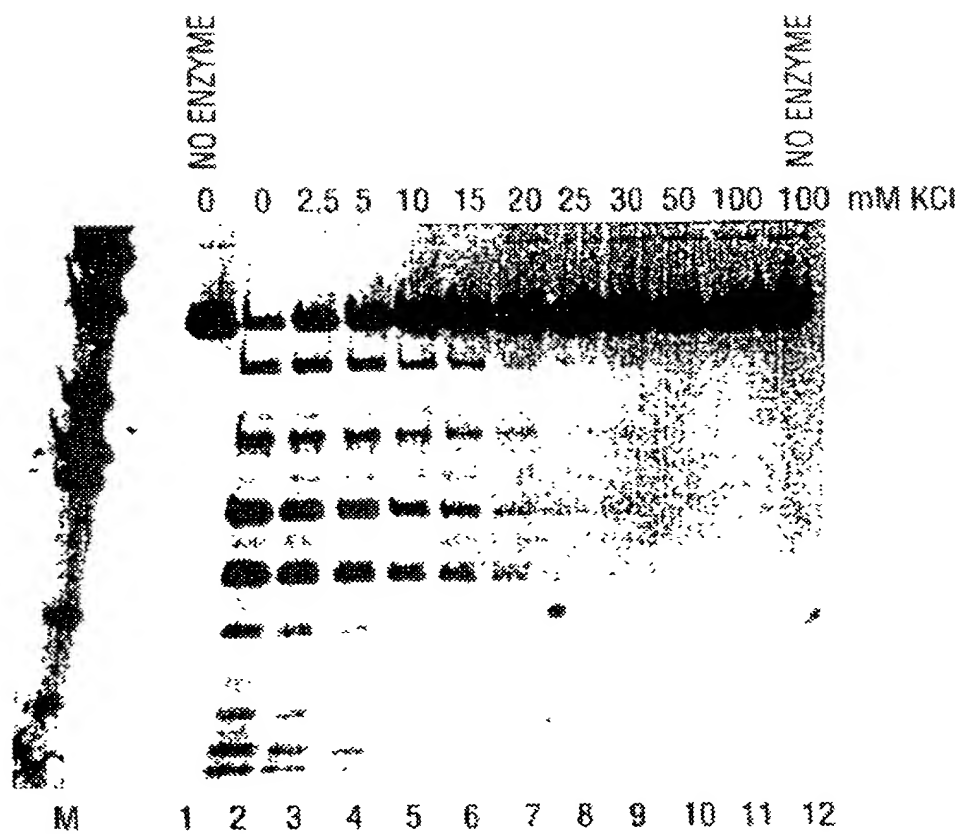


FIG. 57

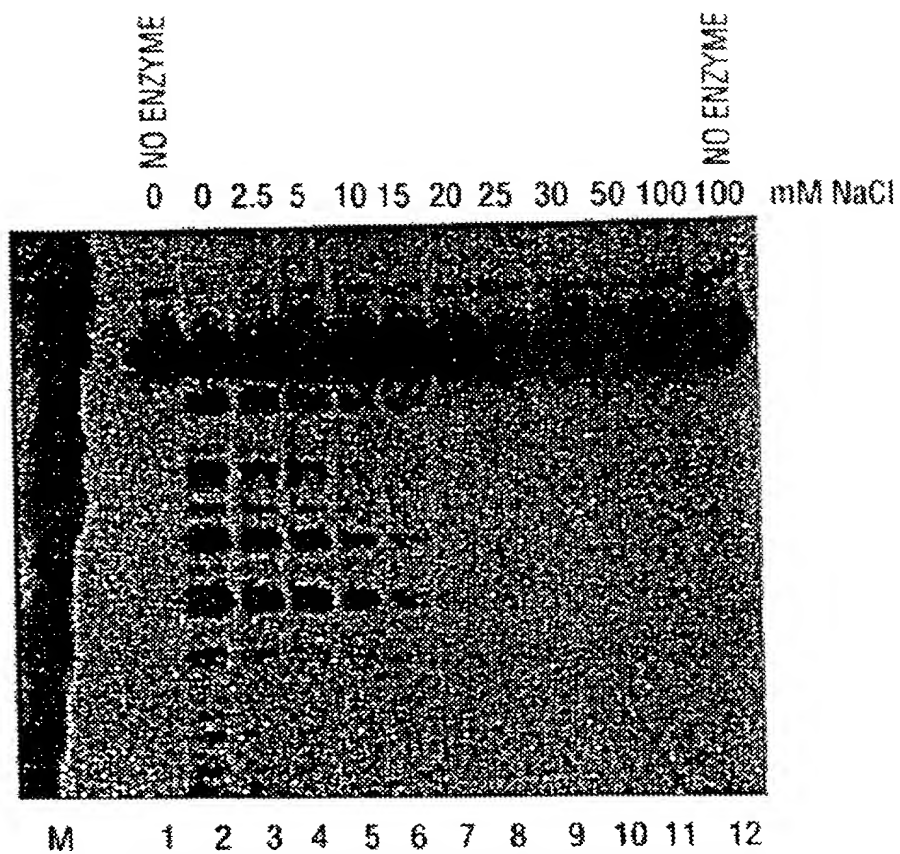


FIG. 58

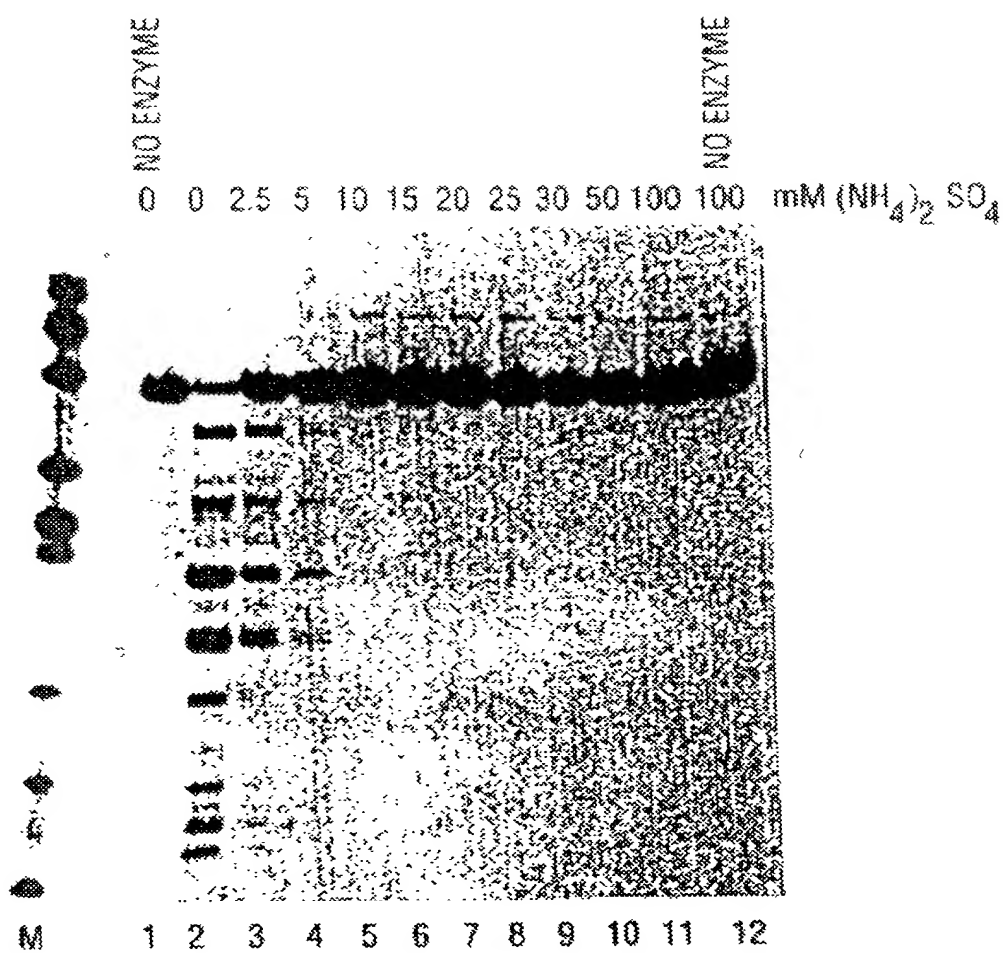


FIG. 59

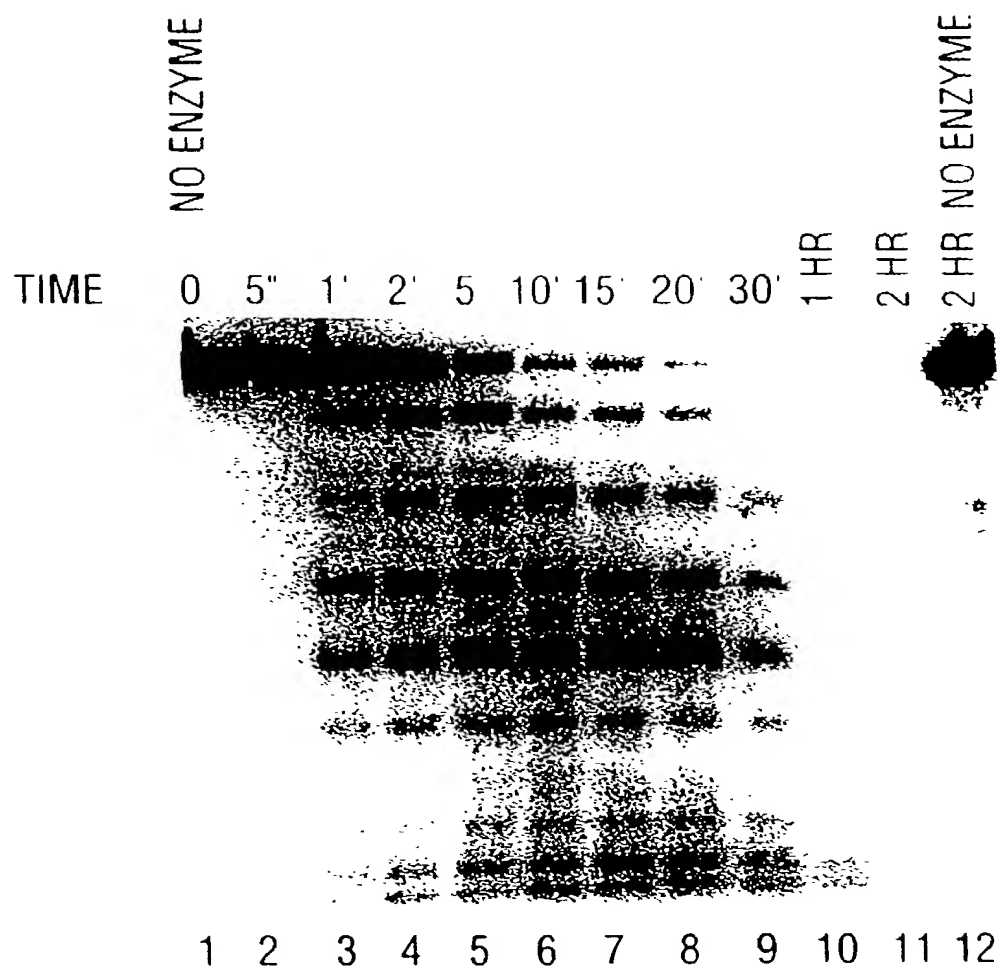


FIG. 60

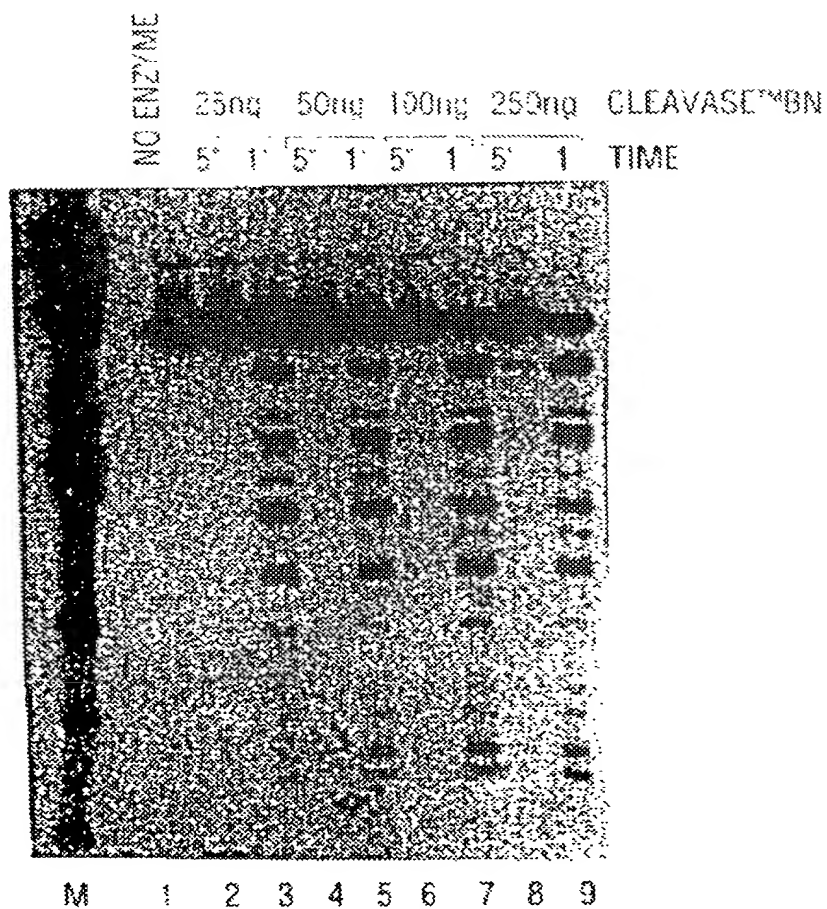


FIG. 61

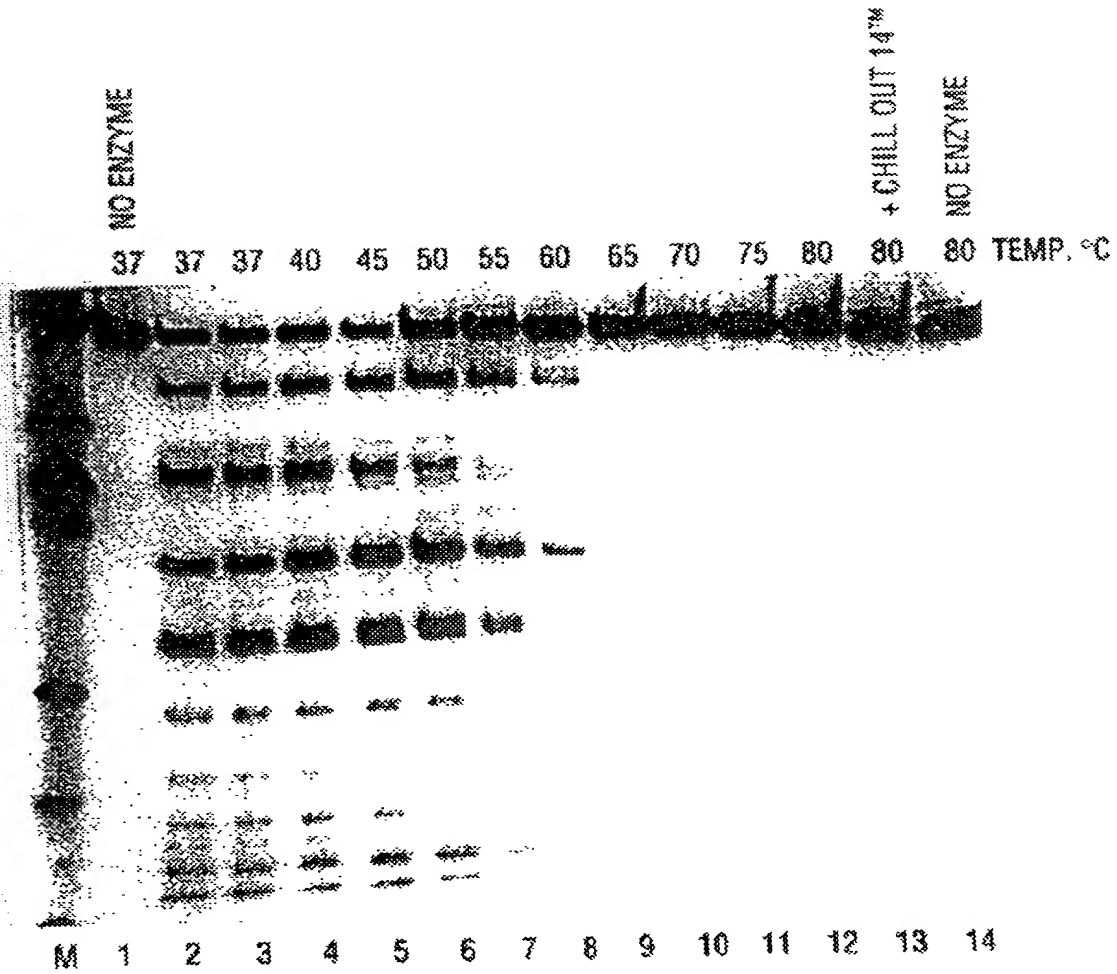


FIG. 62

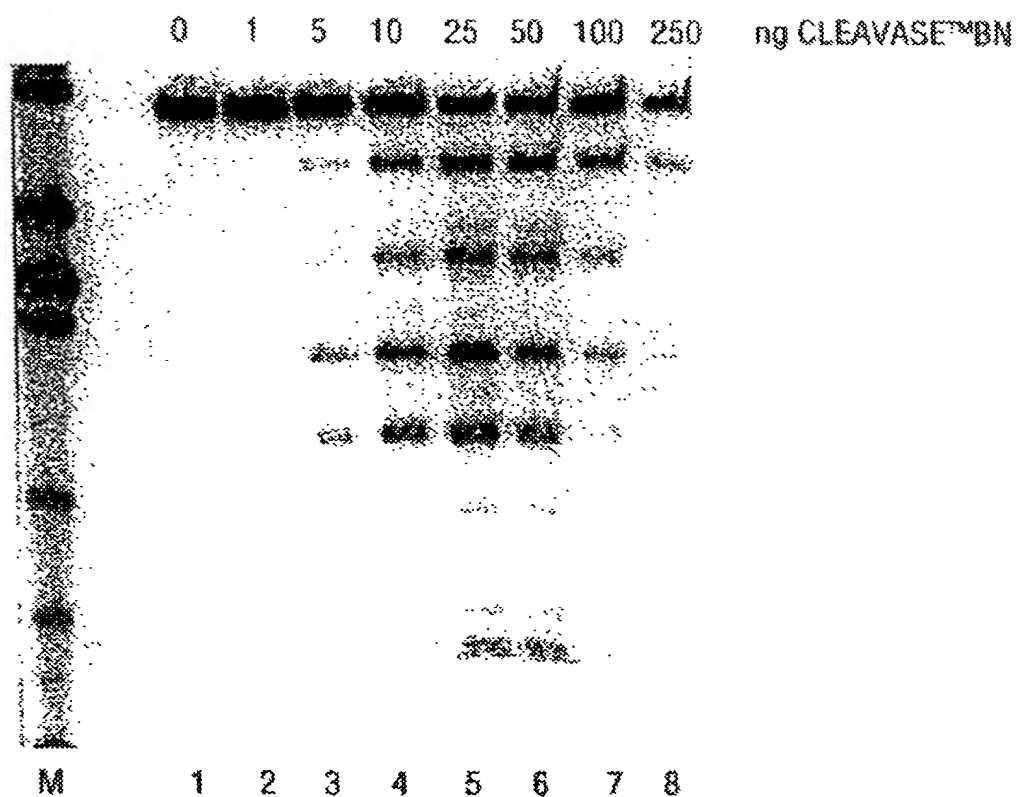


FIG. 63

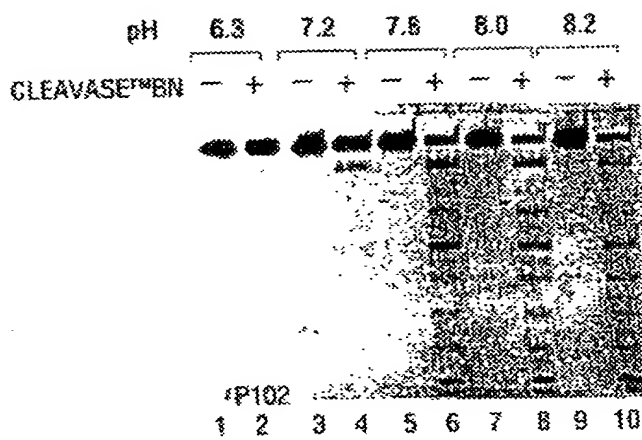


FIG. 64A

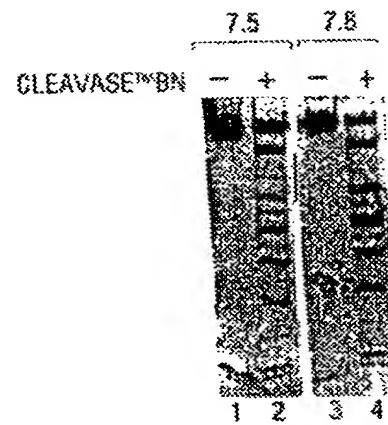
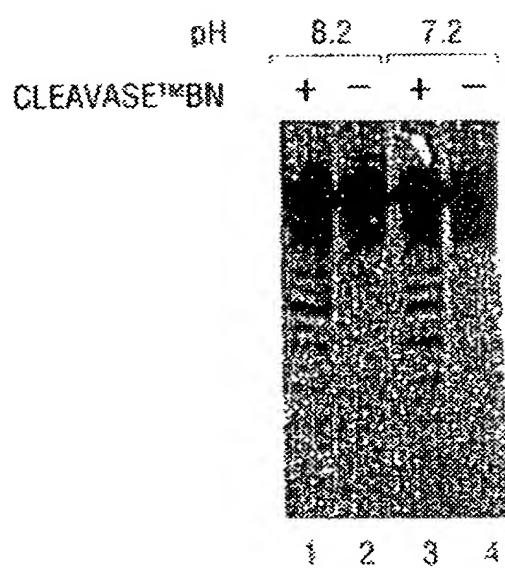


FIG. 64B



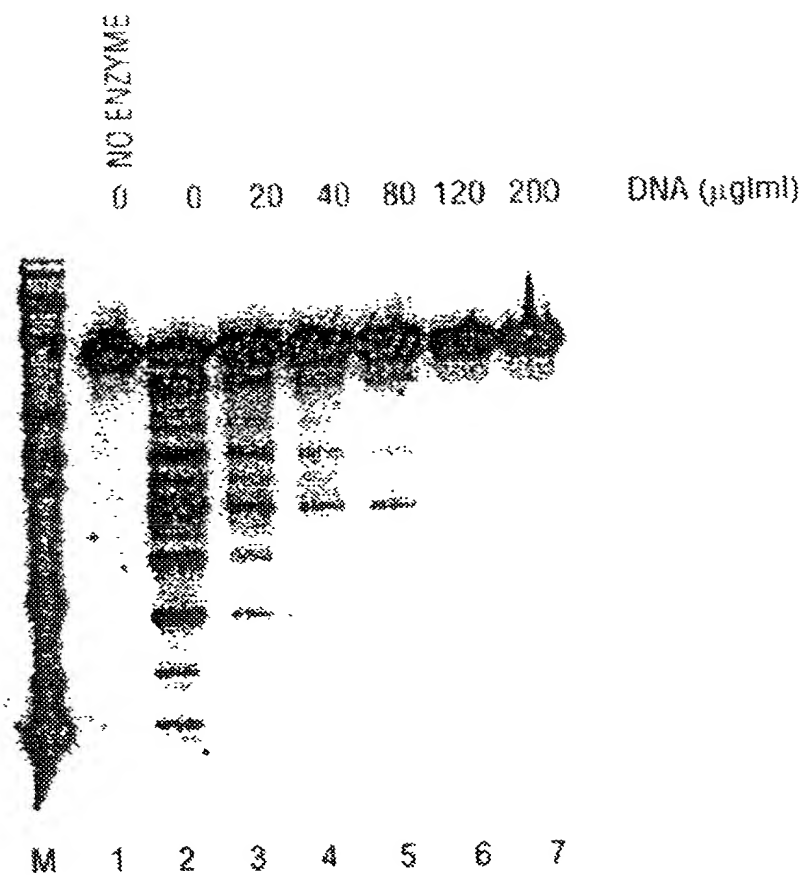


FIG. 66

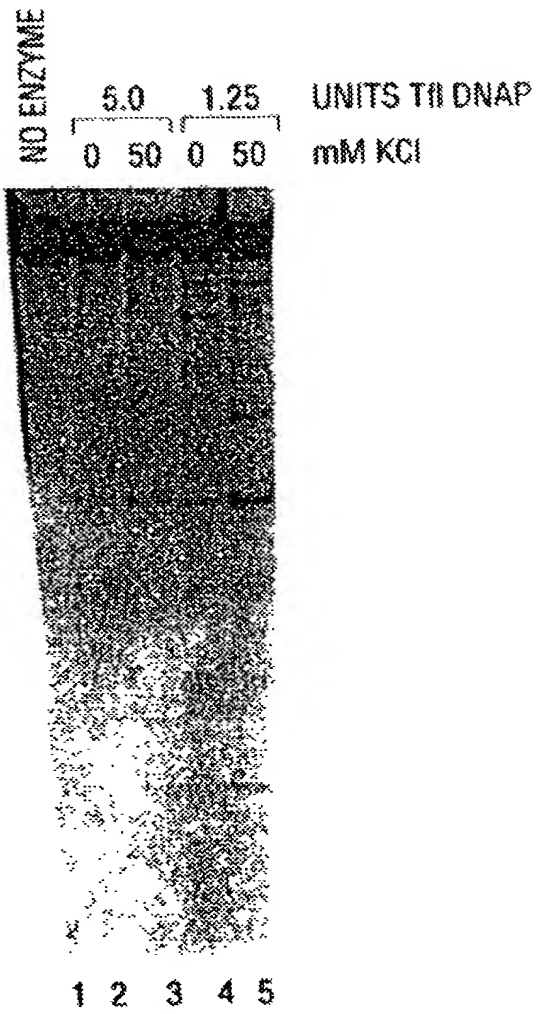


FIG. 67

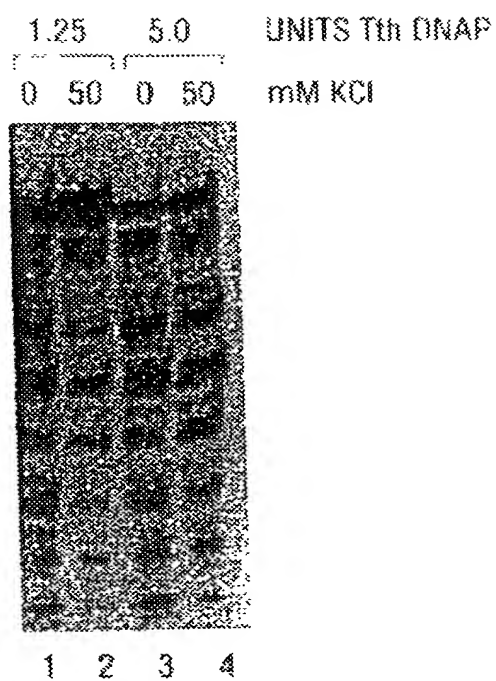


FIG. 68

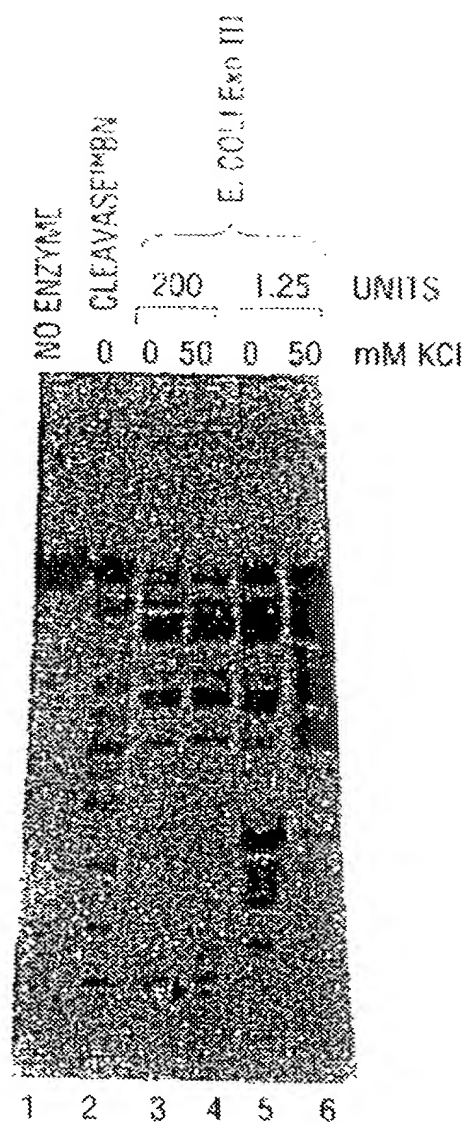


FIG. 69

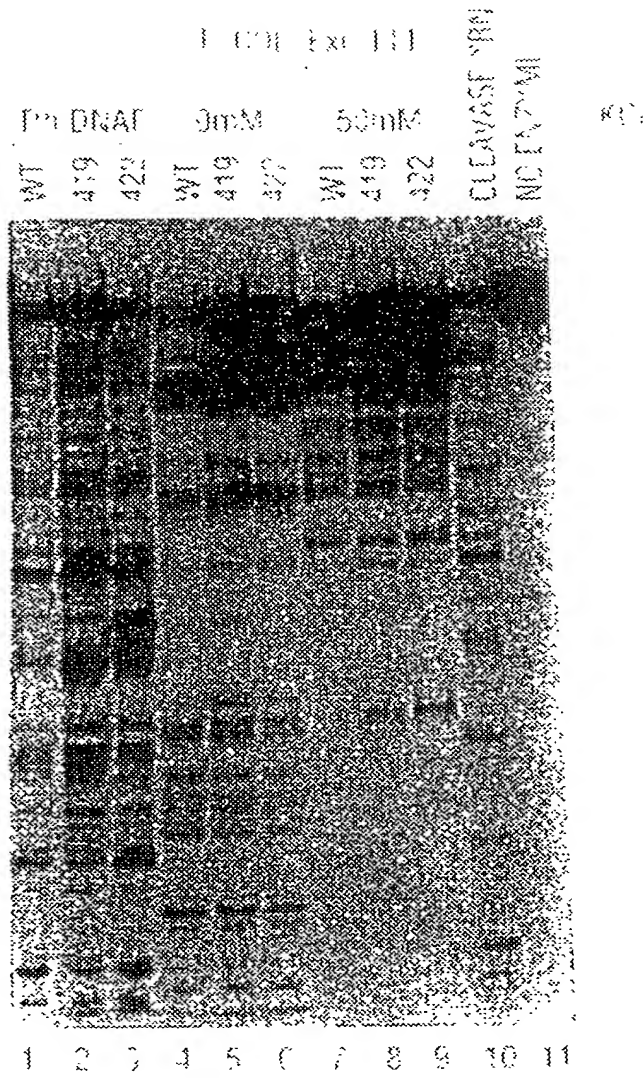
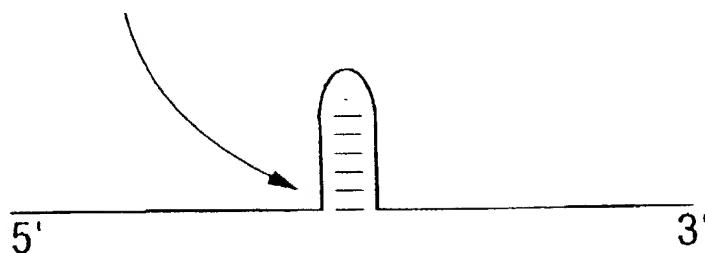


FIG. 70

5' CLEAVAGE SITE



3' CLEAVAGE SITE

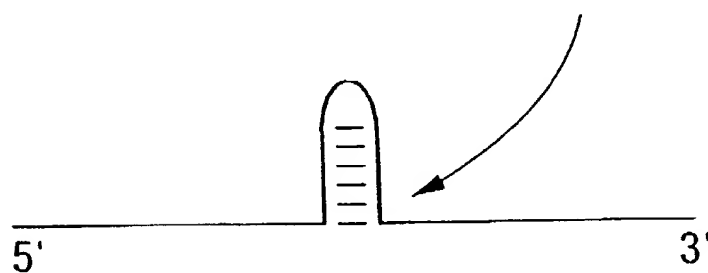


FIG. 71

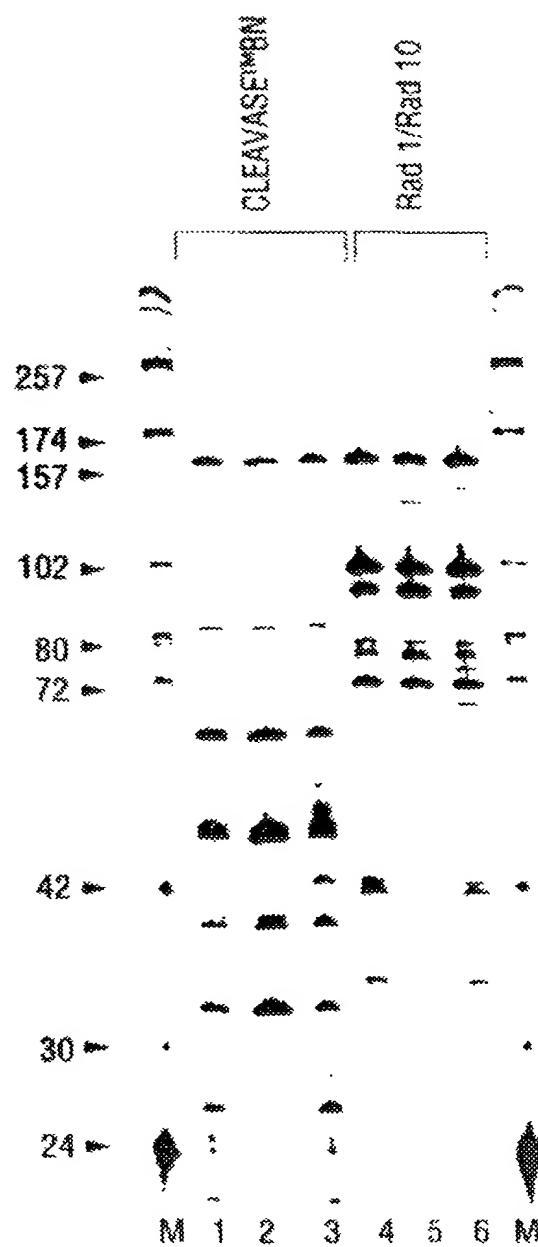


FIG. 72



FIG. 73

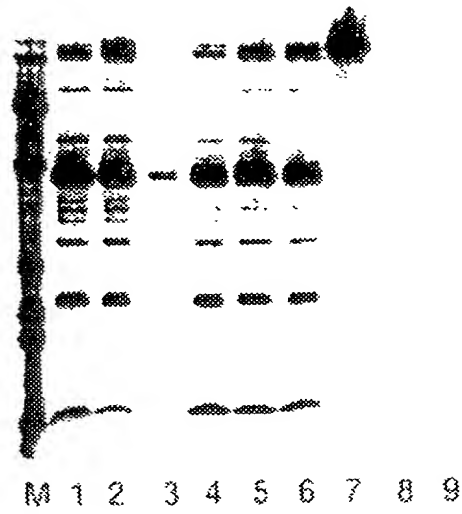
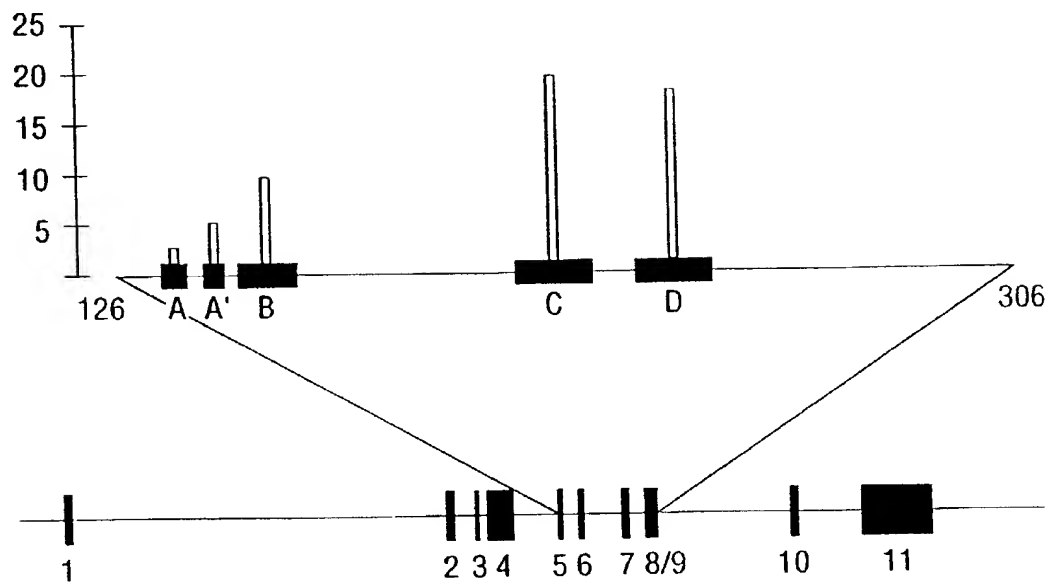


FIG. 75



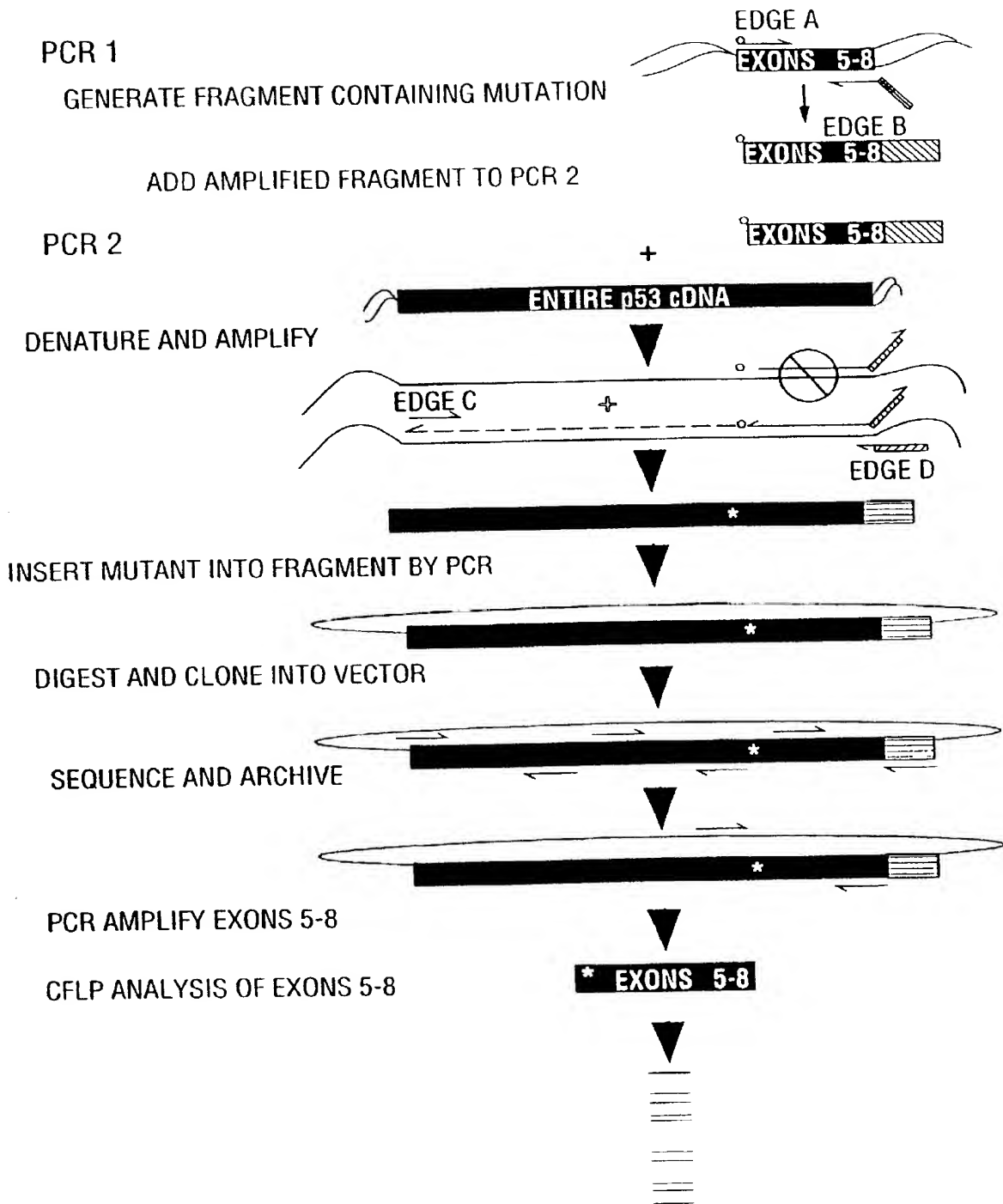


FIG. 77

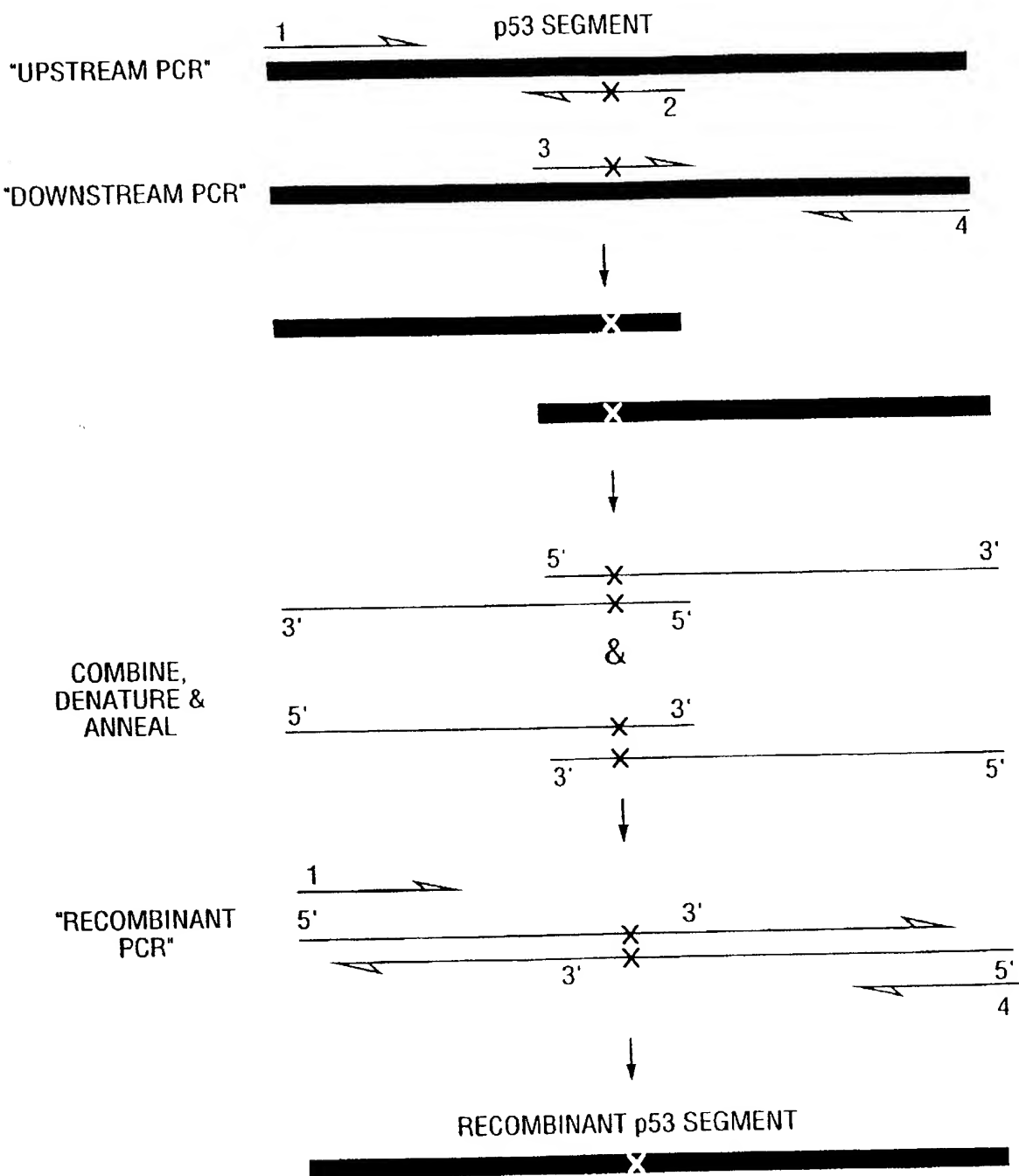


FIG. 78

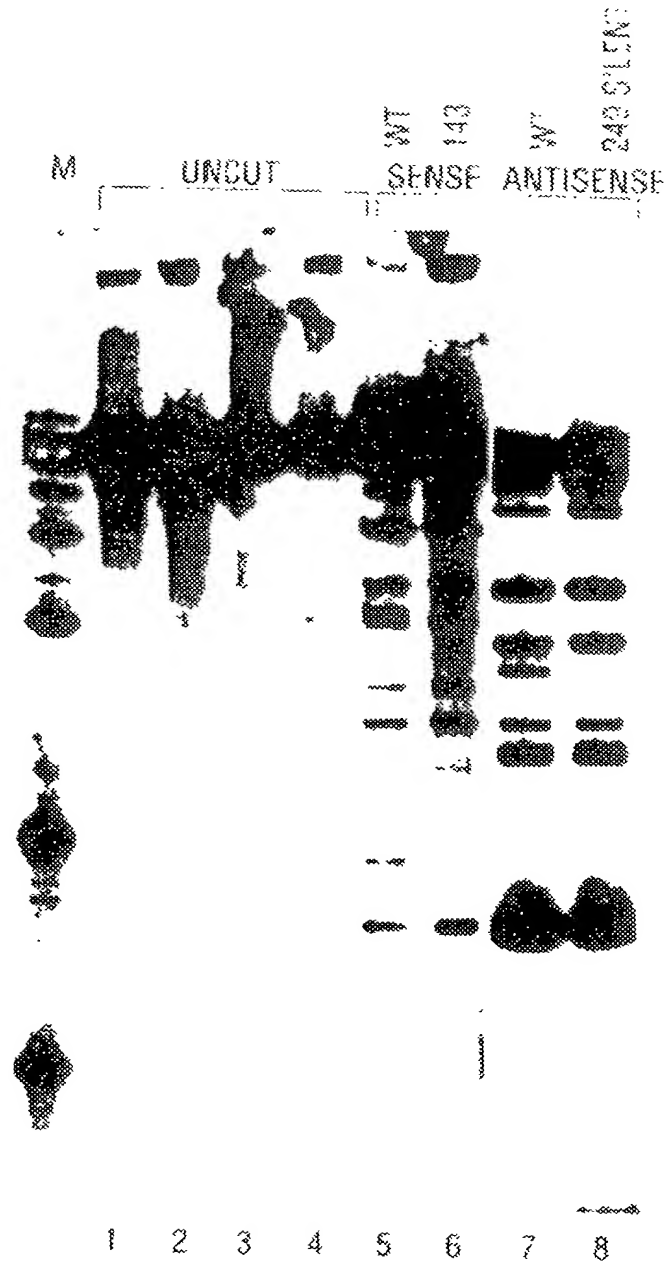


FIG. 79

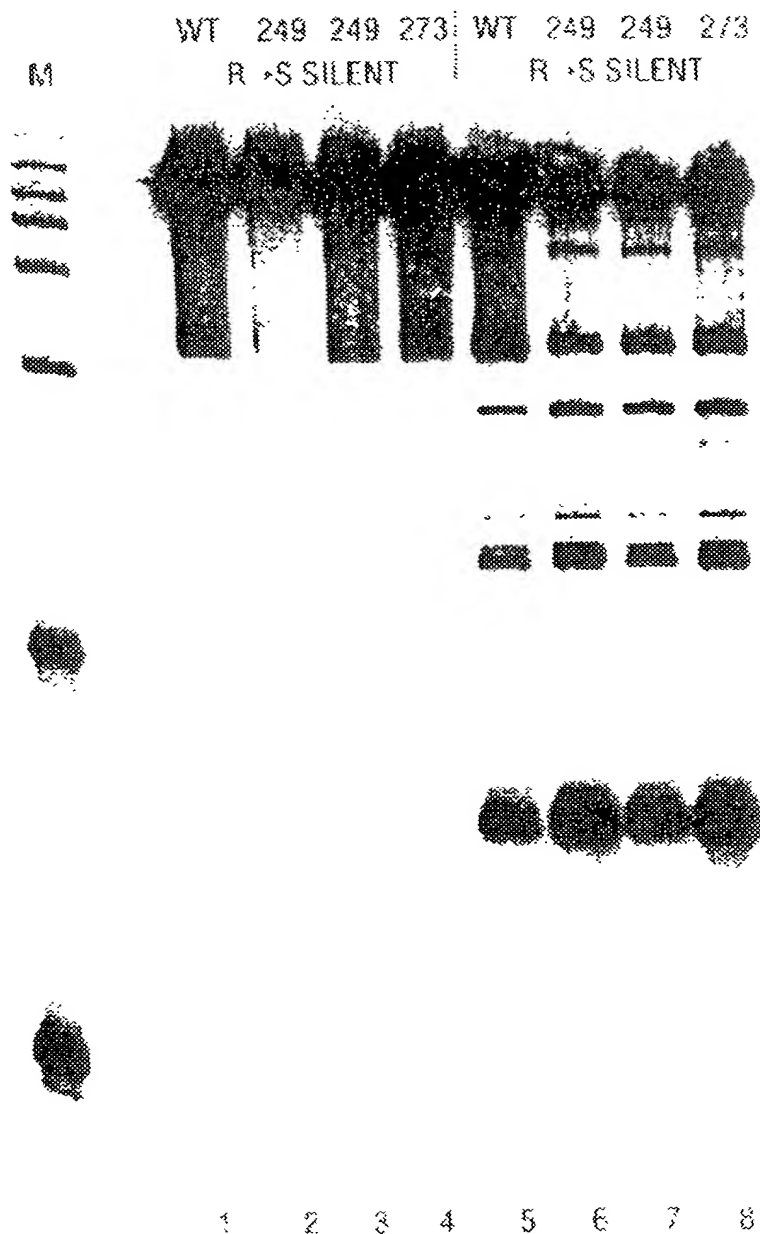


FIG. 80

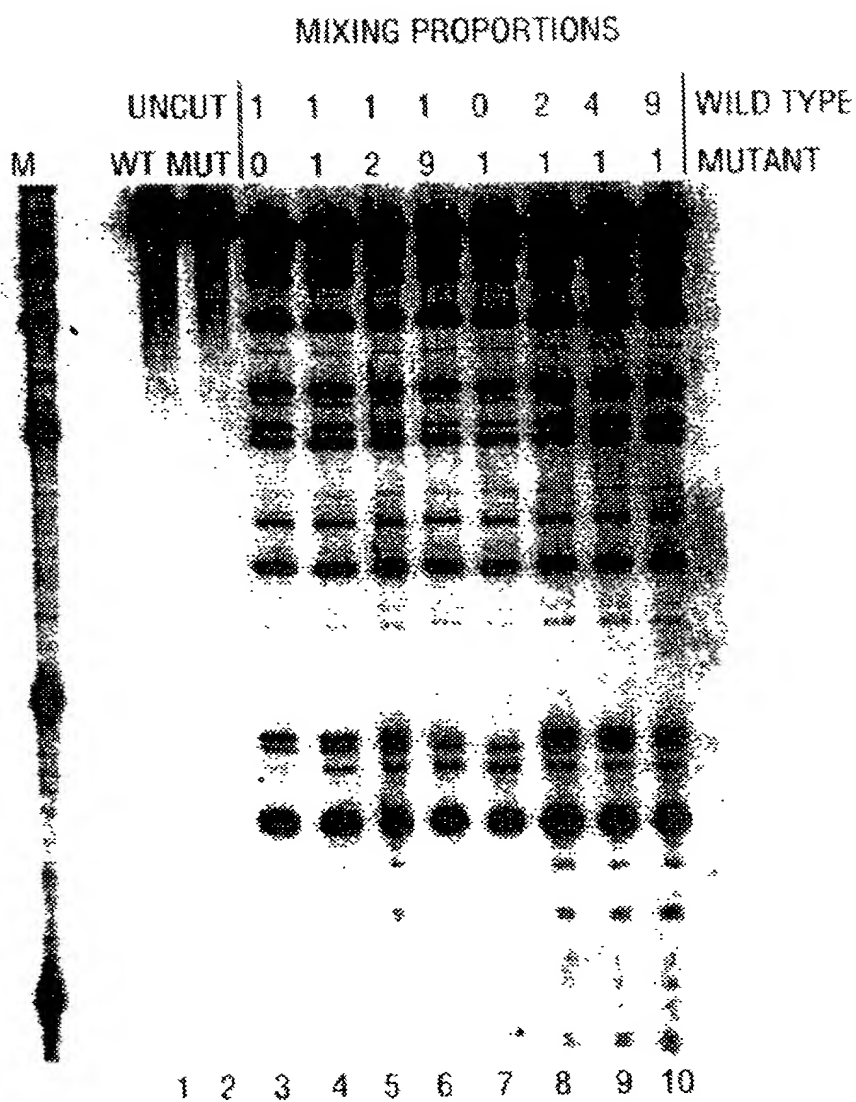


FIG. 81

HCV1.1	(SEQ ID NO:121)	1	CTGTCTTCCAC	GCAGAAAGCG	TCTGGCCATG	GCGTTAGTAT	GAGTGTCTGTG	50
HCV2.1	(SEQ ID NO:122)		CTGTCTTCCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTCTGTG	
HCV3.1	(SEQ ID NO:123)		CTGTCTTCCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTCTGTG	
HCV4.2	(SEQ ID NO:124)		CTGTCTTCCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTCTGTG	
HCV6.1	(SEQ ID NO:125)		CTGTCTTCCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTCTGTG	
HCV7.1	(SEQ ID NO:126)		CTGTCTTCCAC	GCAGAAAGCG	CTAGCCATG	GCGTTAGTAT	GAGTGTCTGTG	
HCV1.1		51	CAGCCTCCAG	GACCCCCCT	CCCGGGAGAG	CCATAGTGGT	CTGCGGAACC	100
HCV2.1			CAGCCTCCAG	GACCCCCCT	CCCGGGAGAG	CCATAGTGGT	CTGCGGAACC	
HCV3.1			CAGCCTCCAG	GACCCCCCT	CCCGGGAGAG	CCATAGTGGT	CTGCGGAACC	
HCV4.2			CAGCCTCCAG	GACCCCCCT	CCCGGGAGAG	CCATAGTGGT	CTGCGGAACC	
HCV6.1			CAGCCTCCAG	GACCCCCCT	CCCGGGAGAG	CCATAGTGGT	CTGCGGAACC	
HCV7.1			CAGCCTCCAG	GACCCCCCT	CCCGGGAGAG	CCATAGTGGT	CTGCGGAACC	
HCV1.1		101	GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGGTCCCTTC	TTGGAT-AAA	150
HCV2.1			GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGGTCCCTTC	TTGGAT-CAA	
HCV3.1			GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGGTCCCTTC	TTGGAT-CAA	
HCV4.2			GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGGTCCCTTC	GTGGATGIAA	
HCV6.1			GGTGAGTACA	CCGGAATTGC	CGGGAAGACT	GGGTCCCTTC	TTGGAT-AAA	
HCV7.1			GGTGAGTACA	CCGGAATCGC	IGGGIGACC	GGGTCCCTTC	TTGGAG-CAA	

FIG. 82A

50 100 150 200 250 300 350 400 450 500 550 600 650 700 750 800 850 900 950 1000

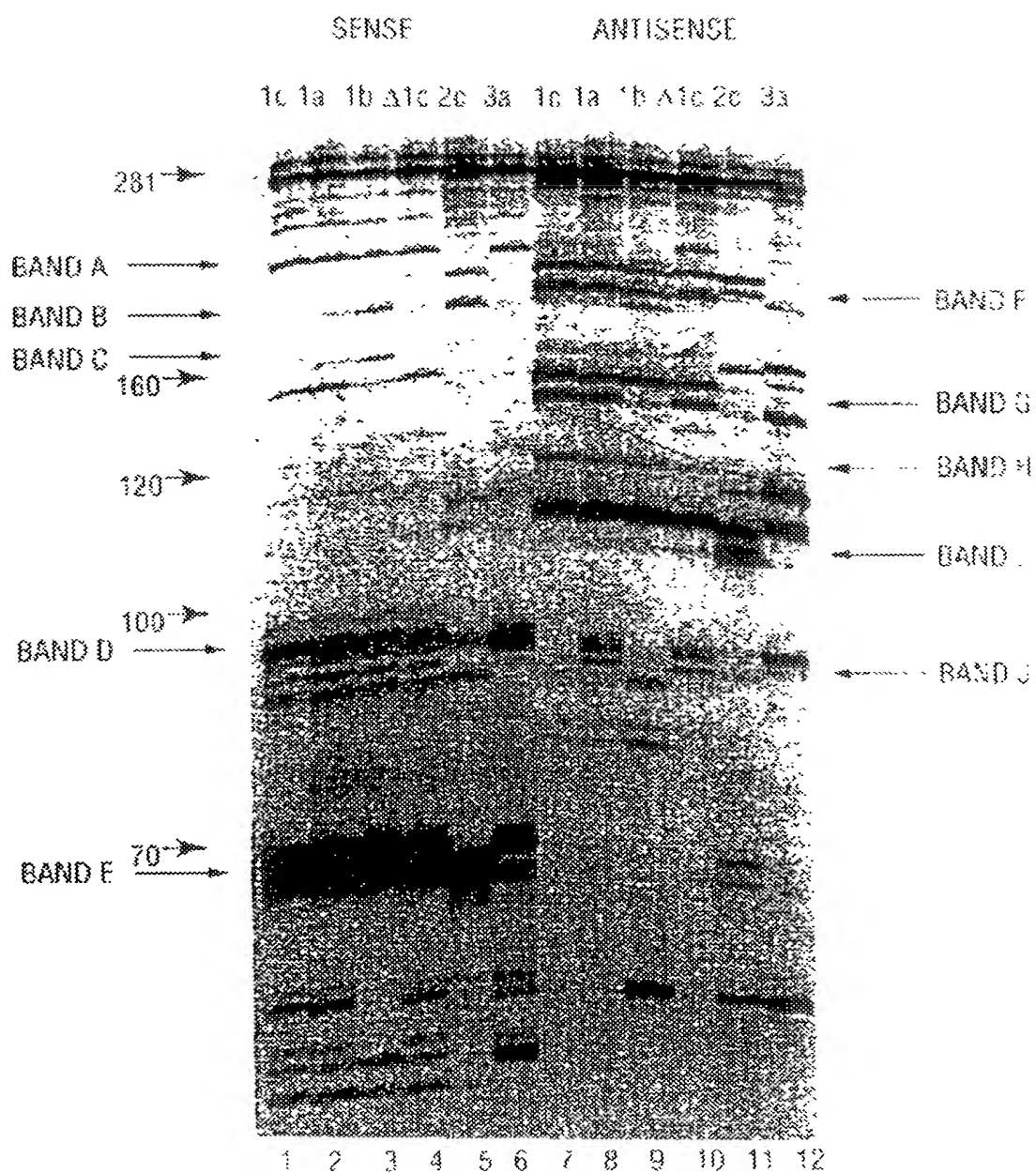


FIG. 83

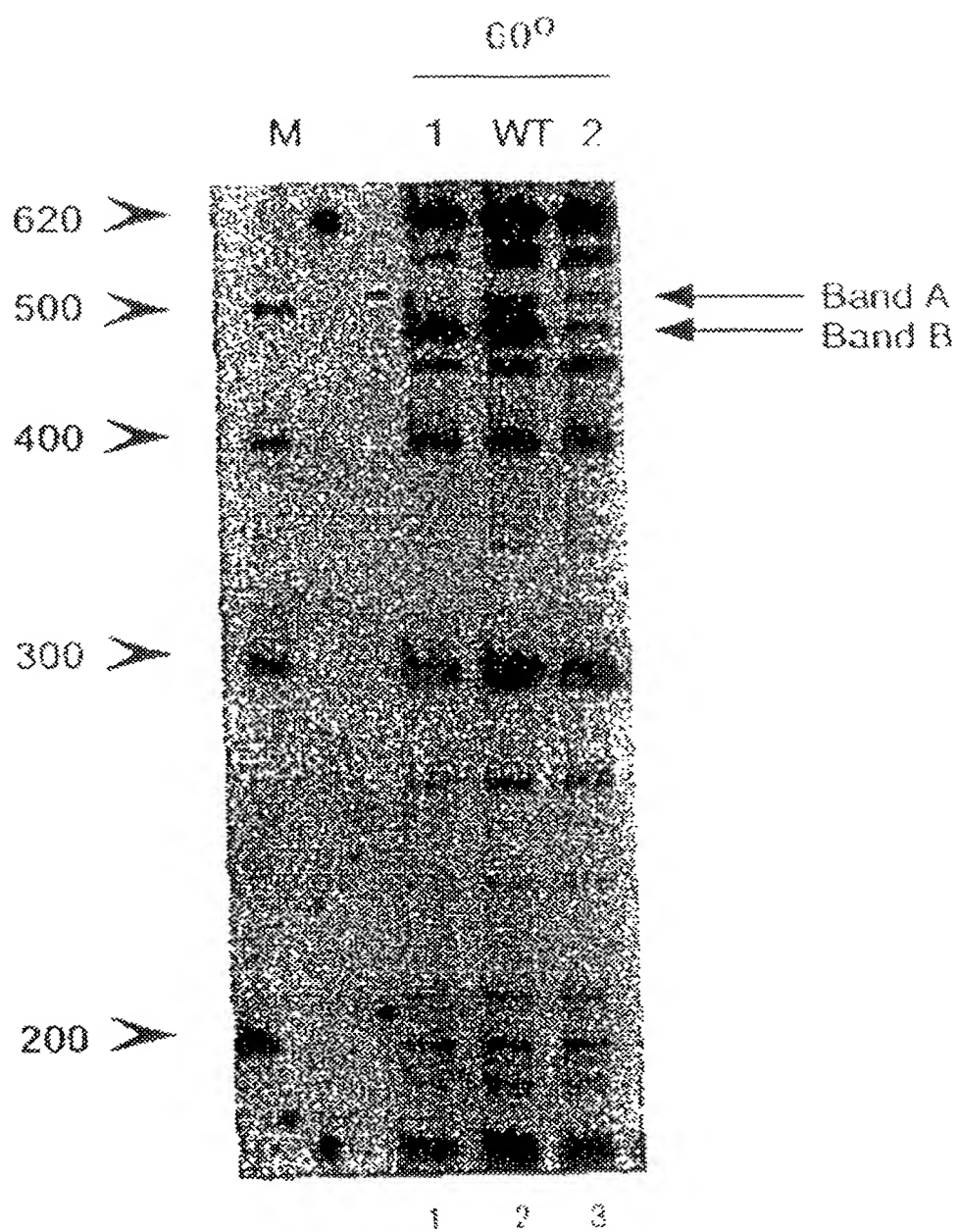


FIG. 84

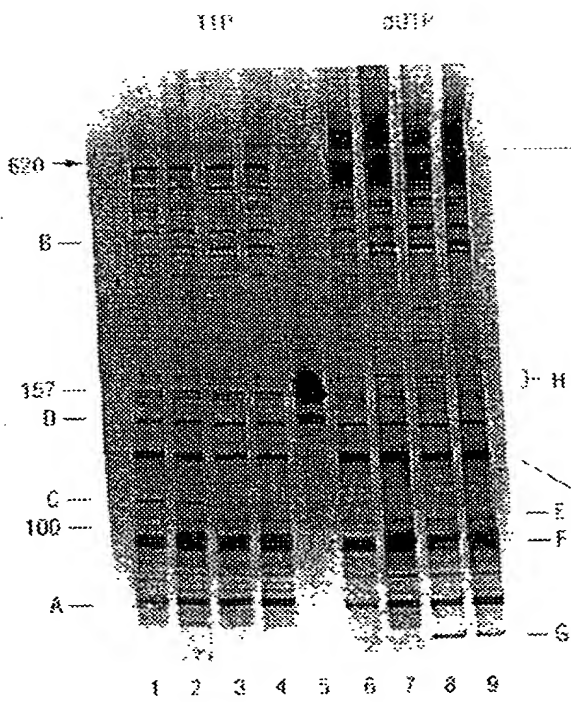


FIG. 85A

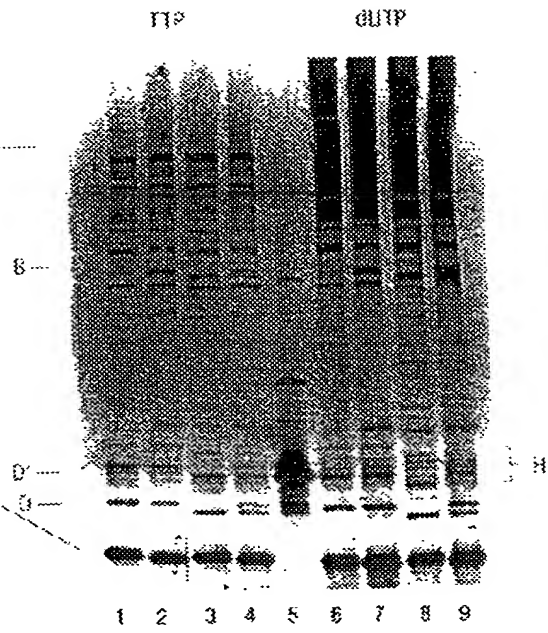


FIG. 85B

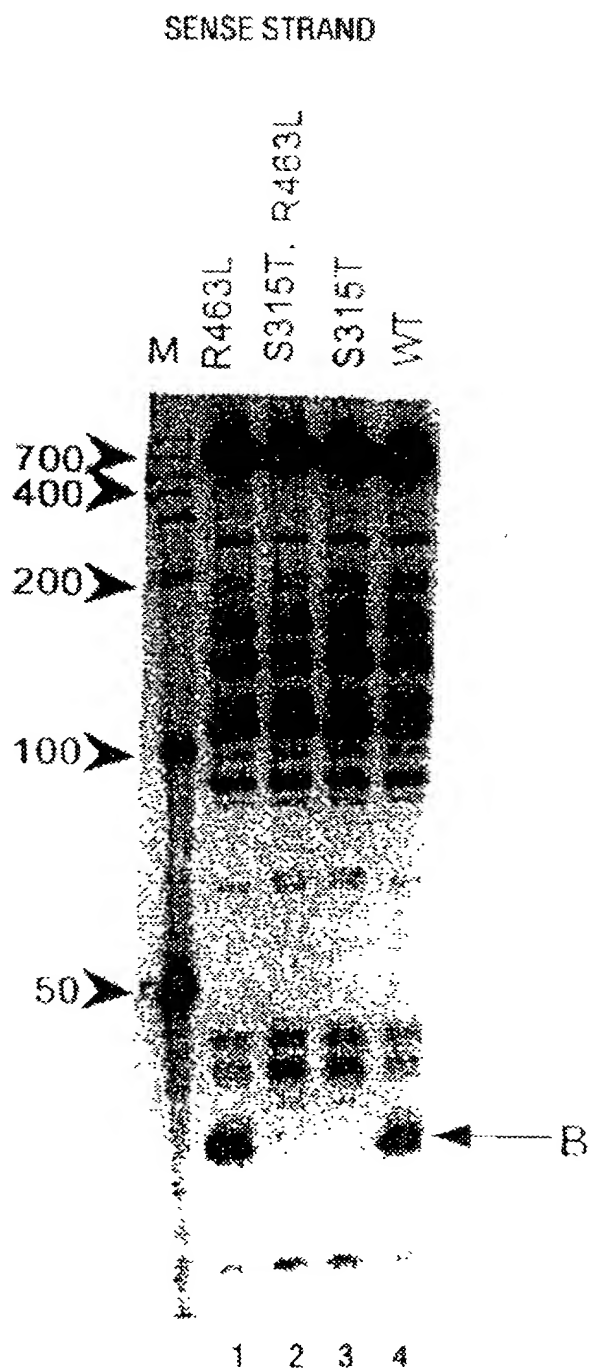


FIG. 86

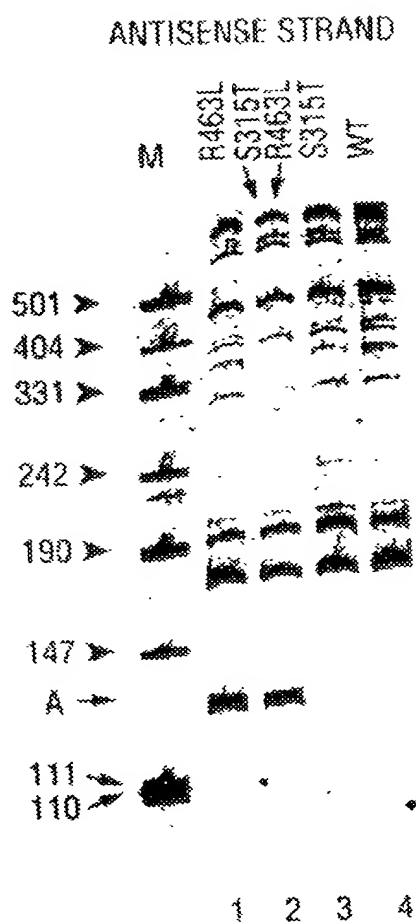


FIG. 87

10	20	30	40	50	60
AGA	GTTTGATCCT	GGCTCAG			
AAATTGAAGA	GTTTGATCAT	<u>GGCTCAGATT</u>	GAAACGCTGGC	GGCAGGCCCTA	ACACATGCAA
TTTAACTTCT	CAAACCTAGTA	CCGAGTCTAA	CTTGCGACCG	CCGTCCGGAT	TGTGTACGTT
1638					
70	80	90	100	110	120
				GGCGGAC	GGGTGAGTAA
GTCGAACGGT	AACAGGAAGA	AGCTTGCTTC	TTTGCTGACG	<u>AGTGGCGGAC</u>	<u>GGGTGAGTAA</u>
CAGCTTGCCA	TTGTCTTCT	TCGAACGAAG	AAACGACTGC	TCACCGCCTG	CCCACCTCATT
130	140	150	160	170	180
TGTCTGGGAA	ACTGCCTGAT	GGAGGGGGAT	AACTACTGGA	AACGGTAGCT	AATACCGCAT
ACAGACCCCT	TGACGGACTA	CCTCCCCCTA	TTGATGACCT	TTGCCATCGA	TTATGGCGTA
190	200	210	220	230	240
AACGTCGCAA	GACCAAAGAG	GGGGACCTTC	GGGCCTCTTG	CCATCGGATG	TGCCCCAGATG
TTGCCAGCGT	CTGGTTTCTC	CCCCTGGAAG	CCCGGAGAAC	GGTAGCCTAC	ACGGGTCTAC
250	260	270	280	290	300
GGATTAGCTA	GTAGGTGGG	TAACGGCTCA	CCTAGGCGAC	GATCCCTAGC	TGGTCTGAGA
CCTAATCGAT	CATCCACCCC	ATTGCCGAGT	GGATCCGCTG	CTAGGGATCG	ACCAGACTCT
310	320	330	340	350	360
GGATGACCCAG	CCACACTGGA	ACTGAGACAC	GGTCCAGACT	CCTACGGGAG	GCAGCAGTGG
CCTACTGGTC	GGTGTGACCT	TGACTCTGTG	<u>CCAGGTCIGA</u>	<u>GGATGCCCTC</u>	<u>CGTCGICACC</u>
1659			TGA	GGATGCCCTC	CGTCGTC

FIG. 88A

1210	1220	1230	1240	1250	1260
ATCATGGCCC	TTA				
ATCATGGCCC	TTACGA				
ATCATGGCCC	TTACGACCAG	GGCTACACAC	GTGCTACAAT	GGCGCATACA	AAGAGAAGCG
TAGTACCGGG	AATGCTGGTC	CCGATGTGTG	CACGATGTTA	CCGCGTATGT	TTCTCTTCGC
1270	1280	1290	1300	1310	1320
ACCTCGCGAG	AGCAAGCGGA	CCTCATAAAG	TGCGTCGTAG	TCCGGATTGG	AGTCTGCAAC
TGGAGCGCTC	TCGTTGCCT	GGAGTATTC	ACGCAGCATC	AGGCCTAACC	TCAGACGTTG
1330	1340	1350	1360	1370	1380
TCGACTCCAT	GAAGTCGGAA	TCGCTAGTAA	TCGTGGATCA	GAATGCCACG	GTGAATACGT
AGCTGAGGTA	CTTCAGCCTT	AGCGATCAAT	AGCACCTAGT	CTTACGGTGC	<u>CACCTTATGCA</u>
				GC	CACCTTATGCA
1390	1400	1410	1420	1430	1440
TCCCGGGCCT	TGTACACACC	GCCCGTCACA	CCATGGGAGT	GGGTTGCAAA	AGAAAGTAGGT
<u>AGGGCCCGGA</u>	<u>ACATGTGTGG</u>	CGGGCAGTGT	GGTACCCCTCA	CCCAACGTTT	TCTTCATCCA
AGGGCCCCGA	ACATG				
1450	1460	1470	1480	1490	1500
AGCTTAACCT	TCGGGAGGGC	GCTTACCACCT	TTGTGATTCA	TGACTGGGGT	GAAGTCGTAA
TCGAAATTGA	AGCCCTCCCG	CGAATGGTGA	AACACTAAGT	ACTGACCCCA	CTTCAGCATT
1510	1520	1530	1540	1550	
CAAGGTAACC	GTAGGGGAAC	CTGCGGTTGG	ATCACCTCCT	TA.....	
GTTCCATTGG	CATCCCCCTG	GACGCCAACC	TAGTGGAGGA	AT.....	

FIG. 88D

```

1638 (SEQ ID NO:151)          AGAGTTTGATCCTGGCTCAG
E.colirrse (SEQ ID NO:158) 0 ...AAATTGAAGAGTTTGATCATGGCTCAGATTGAACGCTGGCGGCAGGCCCTAACACATGCA
Cam.jejun5 (SEQ ID NO:159) 0 ~TTTTTATGGAGAGTTTGATCCCTGGCTCAGAGTGAACGCTGGCGGCGTGCCTAATACATGCA
Stp.aureus (SEQ ID NO:160) 0 ..TTTTATGGAGAGTTTGATCCCTGGCTCAGGATGAACGCTGGCGGCGTGCCTAATACATGCA

ER10 (SEQ ID NO:152)
E.colirrse
Cam.jejun5
Stp.aureus
60 AGTCGAACGGTAACAG----GAAGAAAGCTTGCTTCTTT----GCTGACGAGTGGCGGACGGG
62 AGTCGAACGAT-----GAAGCTTCTAGCTTGCTAGAAAGTGA-----TTAGTGGCGCACGGG
61 AGTCGAGCGAA-----CGGACGAGAAGCTTGCTTCTCTGATG----TT-AGCGGCGGACGGG
GGCGGACGGG

TGAGTAA
114 TGAGTAATGTCTGGGA-AACTGCCTGATGGAGGGGGATAACTACTGGAAACGGTAGCTAATA
114 TGAGTAAGGTATAGTTAATCTGCCCTACACAAGAGGACAACAGTTGGAAACGACTGCTAATA
113 TGAGTAACACGCTGGATAACCTACCTAAGACTGGGATAACTTCGGGAACCGGAGCTAATA
175 CCGCATAAC-----GTCGCAAGAC-----CAAAGAGGGGACCTTTCG-GGCCTCTTG
176 CTCTATACTCCTGCTTAACACAAGTTGAGTAGG-GAAAG-----TTTTT-----CG
175 CCGGATAATATTTTGAACCGCATGGTTCAAAAGTGAAAGACGGT----CTT----GCTGTCA

221 CCATCGGATGTGCCCAGATGGGATTAGCTAGTGGGTAAACGGCTCACCTAGGCGACGA
221 GTGTAGGATGAGACTATATAGTATCAGCTAGTTGGTAAGGTAATGGCTTACCAAGGCTATGA
229 CTTATAGATGGATCCGGCTGCATTAGCTAGTTGGTAAGGTAAACGGCTTACCAAGGCAACGA

283 TCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCCTA
283 CGCTTAACCTGGTCTGAGAGGATGATCAGTCACACTGGAACCTGAGACACGGTCCAGACTCCCTA
291 TACGTAGCCGACCTGAGAGGGGTGATCGGCCACACTGGAACCTGAGACACGGTCCAGACTCCCTA
ACTCCTA
1659 (COMPL)

```

FIG. 89A

1638 1639 1640 1641 1642 1643 1644 1645 1646 1647 1648 1649 1650 1651 1652 1653 1654 1655 1656 1657 1658 1659 1660 1661 1662 1663 1664 1665 1666 1667 1668 1669 1670 1671 1672 1673 1674 1675 1676 1677 1678 1679 1680 1681 1682 1683 1684 1685 1686 1687 1688 1689 1690 1691 1692 1693 1694 1695 1696 1697 1698 1699 1700

E.colirrsE
Cam.jejun5
Stp.aureus
1659 (COMPL)

345 CGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCGCGTG
345 CGGGAGGCAGCAGTAGGGAATATTGCGCAATGGGGAAACCCCTGACGCAGCAACGCCGCGTG
353 CGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGGCGAAAGCCTGACGGAGCAACGCCGCGTG
CGGGAGGCAGCAG

E.colirrsE
Cam.jejun5
Stp.aureus

407 TATGAAGAAGGCCTTCGGGTTGTAAAGTACTTTCAGCGGGGAGGAA-GGGAGTAAAGTTAAT
407 GAGGATGACACTTTTCGGAGCGTAAACTCCTTTTCTTAGGGAAG -----AATT
415 AGTGATGAAGGTCTTCGGATCGTAAACTCTGTTATTAGGGAAGAACATATGTGTAAGTAAC

E.colirrsE
Cam.jejun5
Stp.aureus

468 ACCTTTGCTCATTGACGTTACCCGCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCG
455 C-----TGACGGTACCTAAGGAATAAGCACCGGCTAACTCCGTGCCAGCAGCCGCG
476 -TGTGCACATCTTGACGGTACCTAATCAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCG

FIG. 89B

345 345 353 407 407 415 468 455 476

E.colirrsE	530	GTAATACGGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTTT
Cam.jejun5	506	GTAATACGGAGGGTGCAAGCGTTACTCGGAATCACTGGGCGTAAAGGCGCGTAGGCGGATT
Stp.aureus	538	GTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGCGCGCGTAGGCGGTTT
E.colirrsE	592	GTTAAGTCAGATGTGAAATCCCCGGGCTCAACCTGGGAACTGCATCTGATACTGGCAAGCTT
Cam.jejun5	568	ATCAAGTCTCTTGTGAAATCTAATGGCTTAACCATTAACCTGCTTGGGAACTGATAGTCTA
Stp.aureus	600	TTTAAGTCTGATGTGAAAGCCACGGCTCAACCGTGGAGGCTCATTTGGAACTGGAAACTT
E.colirrsE	654	GAGTCTCGTAGAGGGGGGTAGAAATCCAGGTGTAGCGGTGAAATGCGTAGAGATCTGGAGGA
Cam.jejun5	630	GAGTGAGGGAGAGGCAGATGGAAATTGGTGGTGTAGGGGTAAATCCGTAGATATCACCAAGA
Stp.aureus	662	GAGTGCAGAAAGAGGAAGTGGAATTCATGTGTAGCGGTGAAATGCGCAGAGATATGGAGGA
E.colirrsE	716	ATACCGGTGGCGAAGGGCGGCCCTGGACGAAGACTGACGCTCAGGTGCCGAAAGCGTGGGGA
Cam.jejun5	692	ATACCCATTGCGAAGGCGATCTGCTGGAACTCAACTGACGCTAAGGCGCGAAAGCGTGGGGA
Stp.aureus	724	ACACCAAGTGGCGAAGGCGACTTCTGTGCTGTAACTGACGCTGATGTGCCGAAAGCGTGGGGA
E.colirrsE	778	GCAAACAGGATTAGATACCCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGTGC
Cam.jejun5	754	GCAAACAGGATTAGATACCCCTGGTAGTCCACGCCCTAAACGATGTACACTAGTTGTTGGGGT
Stp.aureus	786	TCAAACAGGATTAGATACCCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAAGTGTTAGGGG

FIG. 89C

530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

<i>E.colirrsE</i>	840	C-CTTGA-GGCGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCCGC
<i>Cam.jejun5</i>	816	G-CTAGT-CATCTCAGTAATGCAGCTAACGCCATTAAGTGTACCGCCTGGGGAGTACGGTCGC
<i>Stp.aureus</i>	848	GT-TTCCGCCCCCTTAGTGCTGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCCG
<i>E.colirrsE</i>	900	AAGGTTAAACTCAAATGAATTGACGGGGGCCCGCACAAAGCGGTGGAGCATGTGTTTAATT
<i>Cam.jejun5</i>	876	AAGATTAAACTCAAAGGAATAGACGGGACCCGCGACAAAGCGGTGGAGCATGTGTTTAATT
<i>Stp.aureus</i>	909	AAGGTTGAACTCAAAGGAATTGACGGGGACCCGCGACAAAGCGGTGGAGCATGTGTTTAATT
<i>E.colirrsE</i>	962	CGATGCAACGCGAAGAACCTTACCTGGTCTTGACATCCACGGAAGTTTTTCAGAGATGAGAAT
<i>Cam.jejun5</i>	938	CGAAGATACGCGAAGAACCTTACCTGGGCTTGATATCCTAAGAACCTTTTTCAGAGATAAGAGG
<i>Stp.aureus</i>	971	CGAAGCAACGCGAAGAACCTTACCAAATCTTGACATCCTTTTGACAACTCTAGAGATAGAGCC
<i>E.colirrsE</i>	1024	GTG--CCTTCGGG--AA-CCGTGAGACAGGTGCTGCATGGCTGTCGTGCTCAGCTCGTGTGTGA
<i>Cam.jejun5</i>	1000	GTGCTAGCTTGCTAGAA-CTTAGAGACAGGTGCTGCACGGCTGTCGTGCTCAGCTCGTGTGTGA
<i>Stp.aureus</i>	1033	TTCC-CCTTCGGG--GGACAAAGTGACAGGTGGTGCATGGTTGTCGTGCTCAGCTCGTGTGTGA
SB-1		GCAACGAGCGCAACCC
<i>E.colirrsE</i>	1081	AATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGGTCCGG-CC
<i>Cam.jejun5</i>	1061	GATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCACGTAATTTAGTTGCTAACGGTTCGG-CC
<i>Stp.aureus</i>	1092	GATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTAAGCTTAGTTGCCATCA-TTAAGT-T

FIG. 89D

GGGTTGGGTTAAGTCCCGCAACGAGCGCAACCC

SB-3 (SEQ ID NO:157)		ATGACGTC AAGTCATC
SB-4 (SEQ ID NO:154)		ATGACGTC AAGTCATC
E.colirrsE	1142	GGGAAC TCAAAGGAGACTGCCAGTGATAAACTGGAGGAAGGTGGGGATGACGTCAAGTCATC
Cam.jejun5	1122	GAGCACTCTAAATAGACTGCCTTCG-TAAGGAGGAGGAAGGTGTGGACGACGTCAAGTCATC
Stp.aureus	1152	GGGCACTCTAAGTTGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAAATCATC
SB-3		ATGGCCCC TTA
SB-4		ATGGCCCC TTACGA
E.colirrsE	1204	ATGGCCCC TTACGACCAAGGGCTACACACGTGCTACAATGGCGCATACAAGAGGACGACCTC
Cam.jejun5	1183	ATGGCCCC TTATGCCCAAGGGCGACACACGTGCTACAATGGCATATAGAAATGAGACGCAATACC
Stp.aureus	1214	ATGGCCCC TTATGATTGGGCTACACACGTGCTACAATGGACAATACAAGGGCAGCGAAACC
E.colirrsE	1266	GCGAGAGCAAGCGGACCTCATAAAGTGCGTCTAGTCCGGATTGGAGTCTGCAACTCGACTC
Cam.jejun5	1245	GCGAGGTGGAG-CAAATCTATAAAATATGTCCCAGTTCGGATTGTTCTCTGCAACTCGAGAG
Stp.aureus	1276	GCGAGGTCAAGCAAATCCCATAAAGTTGTTCTCAGTTCGGATTGTAGTCTGCAACTCGACTA
E.colirrsE	1328	CATGAAGTCGGAATCGCTAGTAATCGTGGATCAGA-ATGCCACGGTGAATACGTTCCCCGGGC
Cam.jejun5	1306	CATGAAGCCGGAATCGCTAGTAATCGTAGATCAGCCATGCTACGGTGAATACGTTCCCCGGGT
Stp.aureus	1338	CATGAAGCTGGAATCGCTAGTAATCGTAGATCAGC-ATGCTACGGTGAATACGTTCCCCGGGT
1743 (compl)		CGGTGAATACGTTCCCCGGGC

FIG. 89E

ATGACGTC AAGTCATC

[illegible]

FIG. 89F

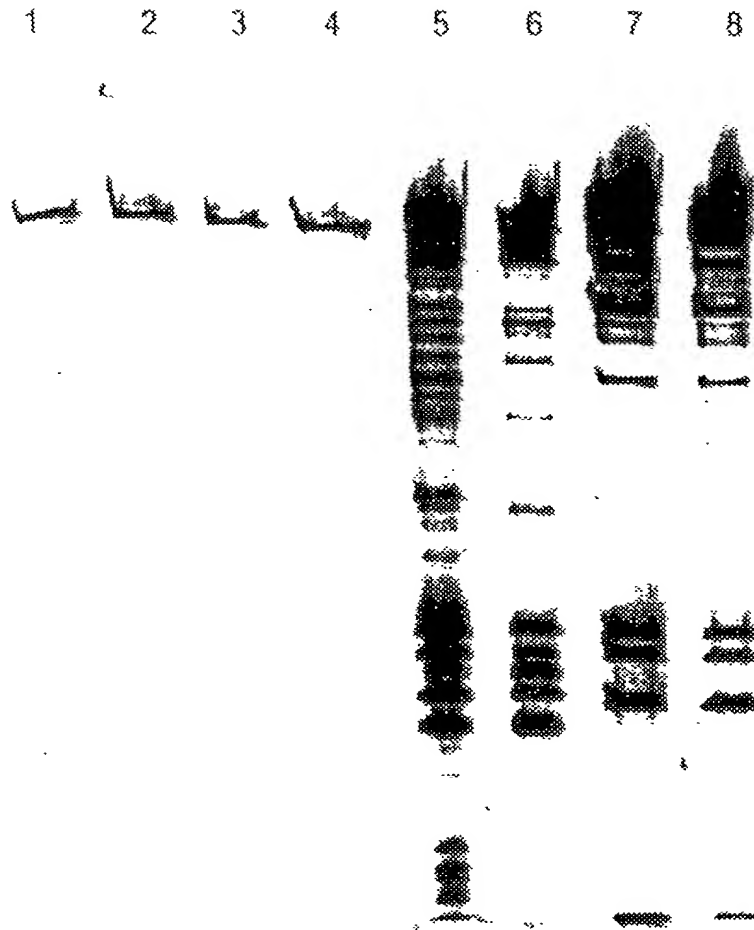


FIG. 90

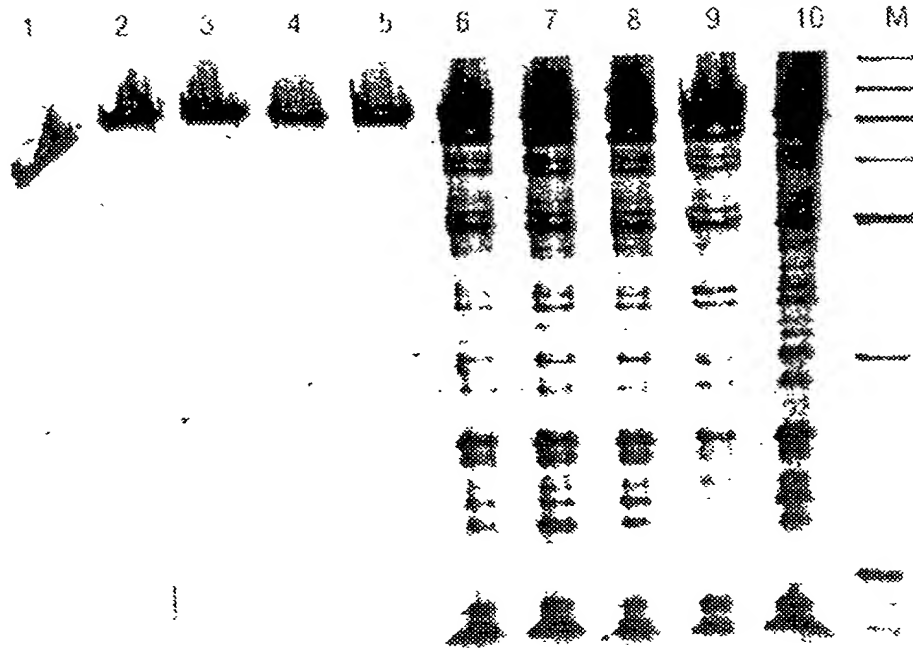


FIG. 91A

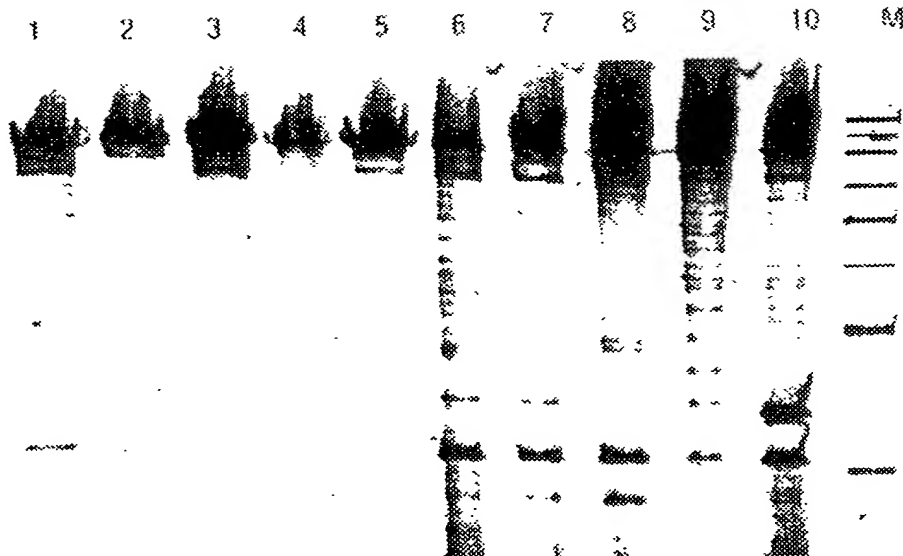


FIG. 91B

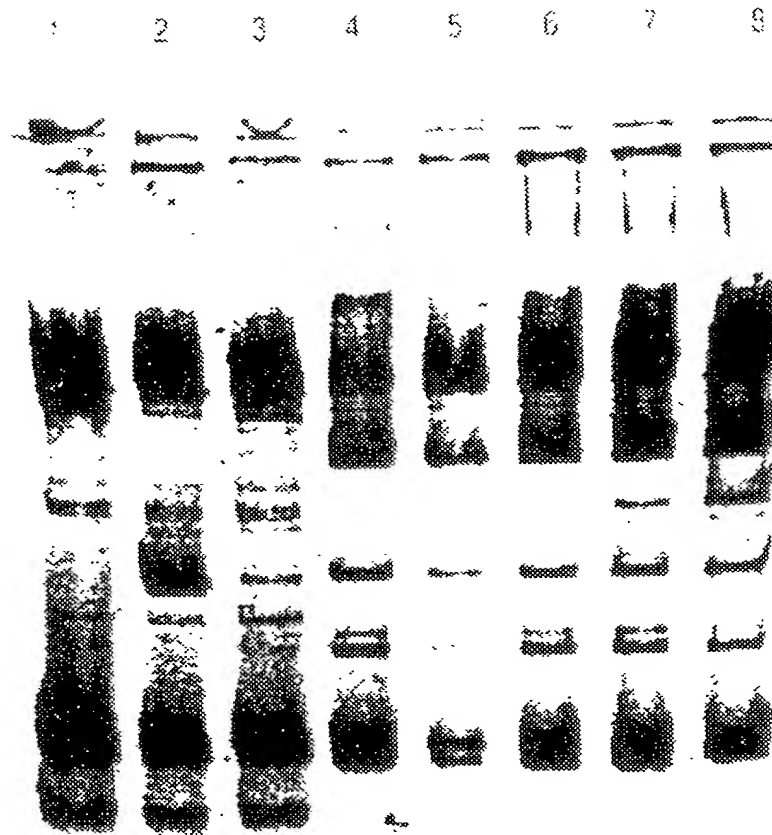


FIG. 93

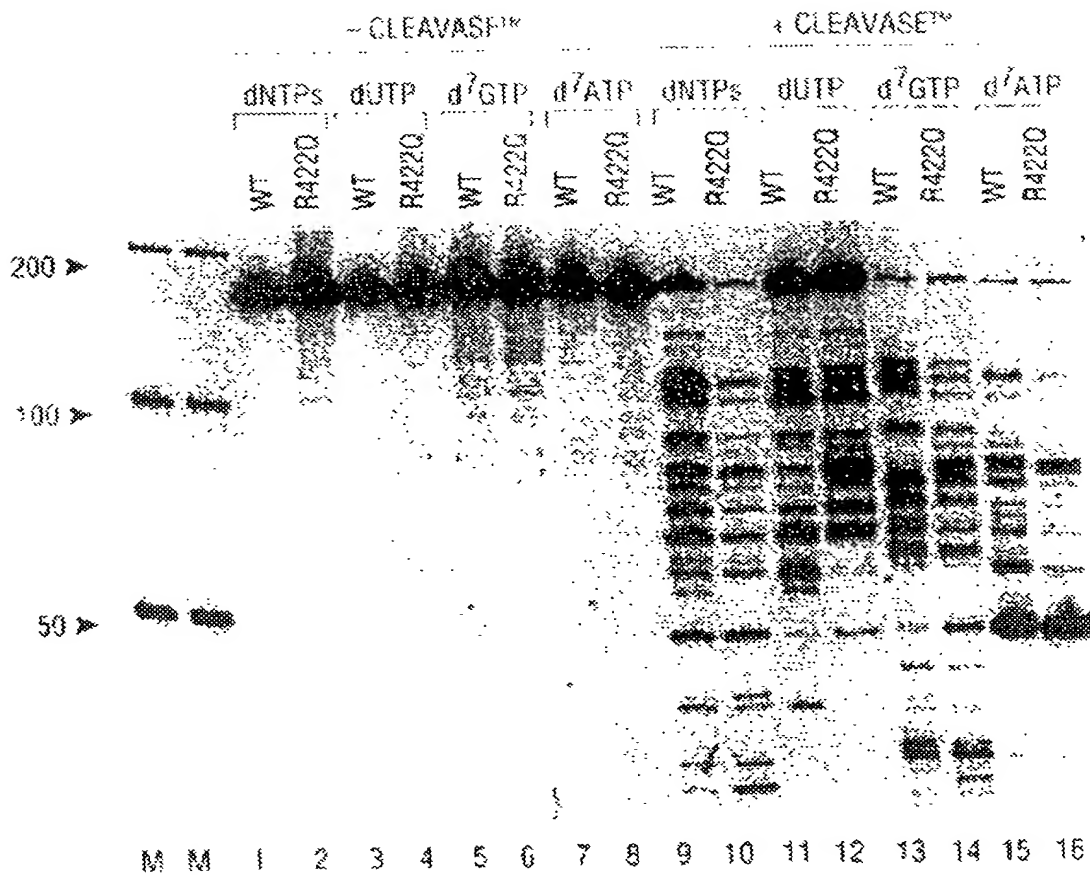


FIG. 94